

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 10, 2005, 23:36:19 ; Search time 1163 Seconds

(without alignments)
92.459 Million cell updates/sec

Title: US-09-553-431b-2

Perfect score: 1654
Sequence: 1 MASLRFTNNHOSLLPSSL.....KAWVBEPPKRGFPSPFGC 326

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1396920 seqs, 329844858 residues

Total number of hits satisfying chosen parameters: 1396920

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : Published Applications AA:*

1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep:*
7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
9: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep:*
10: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep:*
11: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep:*
12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
13: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep:*
14: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep:*
15: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep:*
16: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep:*
17: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep:*
18: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep:*
19: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*
20: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1654	100.0	326	US-10-067-989-1	Sequence 1, Appli
2	1336	80.8	326	US-10-424-599-217748	Sequence 217748,
3	1067.5	64.5	306	US-10-437-963-152399	Sequence 152399,
4	1047	63.3	312	US-10-767-701-39139	Sequence 39139, A
5	792	47.9	284	US-10-067-989-2	Sequence 2, Appli
6	643	38.9	266	US-10-067-989-3	Sequence 3, Appli
7	500.5	30.3	268	US-10-335-977-8662	Sequence 8662, Ap
8	479	29.0	270	US-10-067-989-4	Sequence 4, Appli
9	416	25.2	174	US-10-767-701-58033	Sequence 58033, A
10	351.5	21.3	86	US-10-424-599-219101	Sequence 219101,
11	224	13.5	294	US-10-335-977-9276	Sequence 9276, Ap
12	224	13.5	297	US-10-335-977-9277	Sequence 9277, Ap
13	209	12.6	368	US-10-335-977-7925	Sequence 7925, Ap

14	209	12.6	412	US-10-335-977-7927	Sequence 7927, Ap
15	209	12.6	425	US-10-335-977-7928	Sequence 7928, Ap
16	198	12.0	412	US-10-335-977-7926	Sequence 7926, Ap
17	197.5	11.9	279	US-09-738-626-6925	Sequence 6925, Ap
18	190	11.5	390	US-09-712-363-132	Sequence 192, App
19	179.5	10.9	294	US-10-033-585-7356	Sequence 7356, Ap
20	178	10.8	289	US-10-408-765A-1532	Sequence 1532, Ap
21	178	10.8	319	US-10-112-944-379	Sequence 379, App
22	176	10.6	288	US-09-925-298-730	Sequence 730, App
23	176	10.6	288	US-10-102-806-730	Sequence 730, App
24	174.5	10.6	344	US-10-332-288-2	Sequence 2, Appli
25	173.5	10.5	375	US-09-738-626-4744	Sequence 4744, Ap
26	173.5	10.5	375	US-10-494-672-236	Sequence 236, App
27	173	10.5	355	US-10-424-599-159551	Sequence 159551, A
28	172.5	10.4	377	US-10-156-761-10649	Sequence 10649, A
29	171.5	10.4	338	US-10-282-122A-54123	Sequence 54123, A
30	171	10.3	347	US-10-282-122A-62873	Sequence 62873, A
31	171	10.3	347	US-10-282-122A-64949	Sequence 64949, A
32	170.5	10.3	426	US-10-424-599-170715	Sequence 170715, A
33	169	10.2	351	US-10-282-122A-64065	Sequence 64065, A
34	168.5	10.2	332	US-10-320-797-3108	Sequence 3108, Ap
35	167	10.1	287	US-10-282-122A-45744	Sequence 45744, A
36	164.5	9.9	478	US-09-738-626-3883	Sequence 3883, Ap
37	164	9.9	260	US-10-282-122A-44705	Sequence 44705, A
38	161.5	9.8	478	US-10-494-672-134	Sequence 134, App
39	160	9.7	357	US-10-156-761-11843	Sequence 11843, A
40	159	9.6	349	US-10-282-122A-61836	Sequence 61836, A
41	158.5	9.6	257	US-10-282-122A-65590	Sequence 65590, A
42	154.5	9.3	257	US-10-282-122A-65176	Sequence 65176, A
43	154.5	9.3	348	US-10-767-701-46969	Sequence 46969, A
44	153.5	9.3	257	US-10-282-122A-77571	Sequence 77571, A
45	153.5	9.3	260	US-10-320-797-3069	Sequence 3069, Ap

ALIGNMENTS

RESULT 1
US-10-067-989-1
; Sequence 1, Application US/10067999
; Publication No. US20020144309A1
; GENERAL INFORMATION:
; APPLICANT: Reddy, M.S. Srinivasa
; APPLICANT: Dinkins, Randy
; APPLICANT: Collins, Glenn B.
; TITLE OF INVENTION: Transgenic plants expressing Wind or Mife and an efficient
; FILE REFERENCE: 028750-219
; CURRENT APPLICATION NUMBER: US/10/067,989
; CURRENT FILING DATE: 2002-05-24
; PRIOR APPLICATION NUMBER: US 60/267,488
; PRIOR FILING DATE: 2001-02-09
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 326
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-067-989-1

Query Match 100.0%; Score 1654; DB 13; Length 326;
Best Local Similarity 100.0%; Pred. No. 2e-160;
Matches 326; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MASLRFTNNHOSLLPSSLISQKTLISPRFVNNPSPRISVQFNKKPELAGETPRI 60
Db 1 MASLRFTNNHOSLLPSSLISQKTLISPRFVNNPSPRISVQFNKKPELAGETPRI 60
QY VVTSKGGVGVKTTTANNGLSLARGFSVVAIDALGLRNDLLGLGNRVVYTCVEVI 120
Db VVTSKGGVGVKTTTANNGLSLARGFSVVAIDALGLRNDLLGLGNRVVYTCVEVI 120
QY 61 VVTSKGGVGVKTTTANNGLSLARGFSVVAIDALGLRNDLLGLGNRVVYTCVEVI 120
Db 61 VVTSKGGVGVKTTTANNGLSLARGFSVVAIDALGLRNDLLGLGNRVVYTCVEVI 120
QY 121 NGDCRDLQALVNDKRWSNFELLCISKRSLPLMGFGKALEMLVDLAKTRPEGSDFIIL 180

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Db      121 NGGCRDLQALVADKMSNFELCLSKPSKLPMGFGGKALEMLVDALKTRPESPDII 180
Qy      181 DCPAGIDAGFTAITPANEAVLVTPPDITLADRDVYTGLECGIDIMIVNRRTDM 240
Db      181 DCPAGIDAGFTAITPANEAVLVTPPDITLADRDVYTGLECGIDIMIVNRRTDM 240
Qy      241 IKGEDMSVLDVQEWLGLSLGVIPEDSEVIRSTNRGFPVLNKPPTLAGLAEQAARL 300
Db      241 IKGEDMSVLDVQEWLGLSLGVIPEDSEVIRSTNRGFPVLNKPPTLAGLAEQAARL 300
Qy      301 VEQDSMKAVWVEEPPKRGFFSFFG 326
Db      301 VEQDSMKAVWVEEPPKRGFFSFFG 326

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RESULT 2
US-10-424-599-217748
; Sequence 217748, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J
; APPLICANT: Kovalic, David K
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 217748
; LENGTH: 326
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_38653C.1.pep
US-10-424-599-217748

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Query Match      80.8%; Score 1336; DB 15; Length 326;
Best Local Similarity 80.8%; Pred. No. 7,4e-128;
Matches 269; Conservative 24; Mismatches 26; Indels 14; Gaps 6;

Qy      1 MASIRLP-----STNQSLLPSS--LSQKTLISPPFVNNRSPRSPISVQFNKPEL 53
Db      1 MPSHLPLGATVAPNSTFLLRPHSPPLPSKTL--TKK--KPKPKP--SALFQWNRKDEL 54
Qy      54 AGETPRIVITTSKGGVGGKTTTANGLSARYGSVAIDADLGRNLDLLGLENNRVN 113
Db      55 SSGIPRTVITTSKGGVGGKTTTANGLSARYGSVAIDADLGRNLDLLGLENNRVN 114
Qy      114 YTCVEVINGDCRIDALVDRKMSNFELCLSKPSKLPMGFGGKALEMLVDALKTRPEG 173
Db      115 YTVIEVINDDCRIDALVDRKMSNFELCLSKPSKLPMGFGGKALEMLVDALKTRPEG 174
Qy      174 SPDFIIDCPAGIDAGFTAITPANEAVLVTPPDITLADRDVYTGLECGIDIMIV 233
Db      175 SPDFIIDCPAGIDAGFTAITPANEAVLVTPPDITLADRDVYTGLECGIDIMIV 234
Qy      234 NRVRTDMIKGEDMSVLDVQEWLGLSLGVIPEDSEVIRSTNRGFPVLNKPPTLAGLAF 293
Db      233 NRVRTDMIKGEDMSVLDVQEWLGLSLGVIPEDSEVIRSTNRGFPVLNKPPTLAGLAF 294
Qy      294 EQAARLVQDSMKAVWVEEPPKRGFFSFFG 326
Db      295 EQAARLVQDSMKAVWVEEPPKRGFFSFFG 326

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RESULT 3
US-10-437-963-152399
; Sequence 152399, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:

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; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 152399
; LENGTH: 306
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_52454C.1.pep
US-10-437-963-152399

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Query Match      64.5%; Score 1067.5; DB 16; Length 306;
Best Local Similarity 68.4%; Pred. No. 2.1e-100;
Matches 216; Conservative 31; Mismatches 50; Indels 19; Gaps 5;

Qy      14 LLLPSSLSQKTLISPPFVNNRSPRSPISVQFNKPELAGETPRIVITTSKGGVGT 73
Db      7 LLLPS-----RCPPASPPARHG-----RPAFLSPTRVIVVITTSKGGVGT 51
Qy      74 TTTANVGLSARYGSVAIDADLGRNLDLLGLENNRVNVCVINGDCRIDQALVDR 133
Db      52 TTTANVGLSARYGSVAIDADLGRNLDLLGLENNRVNVCVINGDCRIDQALVDR 133
Qy      134 KRMSNFELCLSKPSKLPMGFGGKALEMLVDALKTRPESPDIIIDCPAGIDAGFTA 193
Db      112 RAHDLQCLSKPSKLPMGFGGKALEMLVDALKTRPESPDIIIDCPAGIDAGFTA 170
Qy      194 ITPANEAVLVTPPDITLADRDVYTGLECGIDIMIVNRRTDMIKGEDMSVLDVQ 253
Db      171 IAPAEAVLVTPPDITLADRDVYTGLECGIDIMIVNRRTDMIKGEDMSVLDVQ 230
Qy      254 EMGLSLGVITDESEVIRSTNRGFPVLNKPPTLAGLAEQAARLVQDSMKAVWEE 313
Db      231 EMGLSLGVITDESEVIRSTNRGFPVLNKPPTLAGLAEQAARLVQDSMKAVWEE 290
Qy      314 E--PKK--GFSEFFG 326
Db      291 QERPCKKAGFFSFFG 306

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RESULT 4
US-10-767-701-39139
; Sequence 39139, Application US/10767701
; Publication No. US20040172684A1
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53535)B
; CURRENT APPLICATION NUMBER: US/10/767,701
; NUMBER OF SEQ ID NOS: 63128
; SEQ ID NO 39139
; LENGTH: 312
; TYPE: PRT
; ORGANISM: Sorghum bicolor
; FEATURE:
; OTHER INFORMATION: Clone ID: SORBI-28WAY03-C93226_1.pep
US-10-767-701-39139

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Query Match 63.3%; Score 1047; DB 16; Length 312;
Best Local Similarity 67.8%; Pred. No. 2.7e-98;
Matches 213; Conservative 33; Mismatches 36; Indels 12; Gaps 5;

15 LPLPSLSOKTIISSPFRVNNPSRRSPISRVLOFNKRPETAGETPRIVITSGSGVGKTT 74
||| : : : : : ||| : : : : :
8 LPLPLPAPAAAPASIRAVS--ARHHGGRTA-----PELSGTPPRVVVITSGSGVGKTT 59
||| : : : : : ||| : : : : :
75 TTANVGLSLARYGSRVAIIDADGLRNLDLLGLENNVNTVEVYINGDCRLDQALVYDK 134
||| : : : : : ||| : : : : :
60 TTANLPAASLARIGLPAVAVADAGLRNLDLLGLENNVNTVEVYINGDCRLDQALVYHR 119
||| : : : : : ||| : : : : :
135 RMSNELICISKPRSKLPMGFGKALEMVLAKTRPESSPFIIIDCPAGIDAGETAI 194
||| : : : : : ||| : : : : :
120 ALQDHLHLCLSPKSKPLAFSGSKTLTWADLRSP--NTPAFIIDCPAGIDAGETAI 178
||| : : : : : ||| : : : : :
195 TPANEAVVTPPTIDALRDADRVTLLEDCGIRDKMTVNRRTIMKGEDMMSVLDVOE 254
||| : : : : : ||| : : : : :
179 APAEAAVLTPTIDALRDADRVAGLLEDCGDKIITVTRPRPLVNGEDMMSVLDVOE 238
||| : : : : : ||| : : : : :
255 MLGSLGLVPEBSEVIRSTNGRPLVINKPPTLAGLAFEOAMRLVEQDSKAAVVEE 314
||| : : : : : ||| : : : : :
229 MLGRLPLGVPEPADAVIRSTNGRPLVINDPPTPALALDQATWRLVERDAMTAVVEEQ 298
||| : : : : : ||| : : : : :
315 --PKKR-GPFSFG 325
||| : : : : : ||| : : : : :
299 ERPKKGGFFSFG 312
||| : : : : : ||| : : : : :

RESULT 5
US-10-067-989-2
; Sequence 2, Application US/10067989
; Publication No. US20020144309A1
; GENERAL INFORMATION:
; APPLICANT: Reddy, M.S. Srinivasa
; APPLICANT: Dinkins, Randy
; APPLICANT: Collins, Glenn B.
; TITLE OF INVENTION: Transgenic plants expressing Wind or Mine and an efficient
; FILE REFERENCE: 028750-219
; CURRENT APPLICATION NUMBER: US/10/067,989
; CURRENT FILING DATE: 2002-05-24
; PRIOR APPLICATION NUMBER: US 60/267,488
; PRIOR FILING DATE: 2001-02-09
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 284
; TYPE: PRT
; ORGANISM: *Chlorella vulgaris*
US-10-067-989-2

Query Match 47.9%; Score 792; DB 13; Length 284;
Best Local Similarity 60.4%; Pred. No. 3e-72;
Matches 165; Conservative 39; Mismatches 55; Indels 14; Gaps 5;

59 RIVVITSGKGVGKTTTANVGLSLARYGSVAIIDADGLRNLDLLGLENNVNTVE 118
||| : : : : : ||| : : : : :
19 RIVVITSGKGVGKTTTANVGLSLARYGSVAIIDADGLRNLDLLGLENNVNTVE 78
||| : : : : : ||| : : : : :
119 VINGDCRLDQALVYDKRMSNFEELLCISKPRSKLPMGFGKALEMVLAKTRPESSPFI 178
||| : : : : : ||| : : : : :
79 IVEGCGCRDQALIRPKRWKNTALLAISKRQK--YVVTTRKNNQNTLDSVK--ELGFGFV 133
||| : : : : : ||| : : : : :
179 IIDCPAGIDAGETAIITPANEAVVTPPTIDALRDADRVTLLEDCGIRDKMTVNRRT 238
||| : : : : : ||| : : : : :
134 LIDCPAGIDVGRINAIASQEAIVITPEITAIARDADRVAGLLEANGIYVNLVNRVP 193
||| : : : : : ||| : : : : :
239 DMKGEDMMSVLDVOEMLGSLGLVPEBSEVIRSTNGRPLVINKPPTLAGLAFEOAAM 298
||| : : : : : ||| : : : : :
194 DMIGKNDMMSVLDVOEMLGSLGLVPEBSEVIRSTNGRPLVINKPPTLAGLAFEOAAM 253
||| : : : : : ||| : : : : :
299 RLIV-EQDSKAAVVEEERPKKGGFFSFG 326
||| : : : : : ||| : : : : :

[illegible]

```

/      SOFTWARE: UNIX
/      CURRENT APPLICATION DATA:
/      APPLICATION NUMBER: US/10/335.977
/      FILING DATE: 30-DEC-2002
/      PRIOR APPLICATION DATA:
/      APPLICATION NUMBER: 08/993.002
/      FILING DATE: 17-DEC-1997
/      ATTORNEY/AGENT INFORMATION:
/      NAME: Mandragoras, Amy E.
/      REGISTRATION NUMBER: 36,207
/      REFERENCE/DOCKET NUMBER: GTN-018
/      TELECOMMUNICATION INFORMATION:
/      TELEPHONE: (617) 227-7400
/      TELEFAX: (617) 742-4214
/      INFORMATION FOR SEQ ID NO: 8662:
/      SEQUENCE CHARACTERISTICS:
/      LENGTH: 268 amino acids
/      TYPE: amino acid
/      TOPOLOGY: linear
/      MOLECULE TYPE: protein
/      HYPOTHEICAL: YES
/      ORIGINAL SOURCE:
/      ORGANISM: Helicobacter pylori
/      FEATURE:
/      NAME/KEY: misc feature
/      LOCATION: (8) LOCATION 1...268
/      SEQUENCE DESCRIPTION: SEQ ID NO: 8662:
/
US-10-335-977-8662
/
Query Match      30.3%; Score 500.5; DB 15; Length 268;
Best Local Similarity 39.8%; Pred. No. 1.9e-42;
Matches 109; Conservative 65; Mismatches 81; Indels 19; Gaps 5;

QY 60 IVVTSGGKGVKTTTANVGLSLARYGFSVAIDADLGRNLDLIGLERNVYTCVE 119
DB 4 VVTISGKGVKTTTANVGLSLARYGFSVAIDADLGRNLDLIGLERNVYTCVE 119
QY 120 INDCRDLQALVRDKRNSFELLCSKPSKRLPMGFGKALEWLVVALKTRPGSPDFI 179
DB 64 MEKCNLSQALITDKTKLSFLAASGSKOKNLDREKVAI--LINALR---ADPDYL 117
QY 180 IDCAGIDAGFTITPANEAVLVTPDITARDADRTGLLECDSIR-----DIKAI 232
DB 118 IDSPAGIESGFEHALHLDALVVTPEVSLSDSRVIGIIDAKSNRAKSGEEVHKHLI 177
QY 233 VNRRTDMIKGEDMNSVLDOEMLGSLGVIPEDSEVIRSTNRGFPPLVANKPPTLAGI 292
DB 178 INLKEELVANGSMISIEVLKILCLPLIGIIPEDHIIISATNKGEPIV--RTDCESAKA 235
QY 293 FEQAAWRLVEQDSMKAVWVEEPKRGFPFSG 326
DB 236 YORITRRIIGEE---VEYVEFKAKRGFPFSAKLG 265

RESULT 8
US-10-067-989-4
/ Sequence 4; Application US/10067989
/ Publication No. US20020144309A1
/ GENERAL INFORMATION:
/ APPLICANT: Dinkins, Randy
/ APPLICANT: Reddy, M.S. Srinivasa
/ TITLE OF INVENTION: Transgenic plants expressing MIND or MIND and an efficient
/ FILE OF INVENTION: method for plant chloroplast transformation and gene expression
/ FILE REFERENCE: 028750-219
/ CURRENT APPLICATION NUMBER: US/10/067.989
/ PRIOR FILING DATE: 2002-05-24
/ PRIOR APPLICATION NUMBER: US 60/267,488
/ NUMBER OF SEQ ID NOS: 18
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 4
/ LENGTH: 270

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/      TYPE: PRT
/      ORGANISM: Escherichia coli
/      US-10-067-989-4
/
Query Match      29.0%; Score 479; DB 13; Length 270;
Best Local Similarity 39.9%; Pred. No. 3.1e-40;
Matches 113; Conservative 58; Mismatches 82; Indels 30; Gaps 8;

QY 59 RIVVTSGKGVKTTTANVGLSLARYGFSVAIDADLGRNLDLIGLERNVYTCVE 118
DB 3 RIVVTSGKGVKTTTANVGLSLARYGFSVAIDADLGRNLDLIGLERNVYTCVE 118
QY 119 VINGCDRLQALVRDKRNSFELLCSKPSKRLPMGFGKALEWLVVALKTRPGSPDFI 178
DB 63 VINGCDRLQALVRDKRNSFELLCSKPSKRLPMGFGKALEWLVVALKTRPGSPDFI 178
QY 179 IIDCPAGIDAGFTITPANEAVLVTPDITARDADRTGLLEC-----DGIRDIK-- 230
DB 118 VCDSPAGIETGALMALYFADRAITITNPEVSSVRSDRIIGILASKSRRAENGEBPIKEH 177
QY 231 MIVNRRTDMIKGEDMNSVLDOEMLGSLGVIPEDSEVIRSTNRGFPPLVANKPPTLAG 290
DB 178 ILITRYNPGRVSRGDMLEMDVLEIRIKLVGVIPEDQSVLRASNGEPIVLDINAD-AG 236
QY 291 LAFEQAAWRLVEQDSMKAVWVEEP-----KRGFPF--FPGG 326
DB 237 KAY-----ADYERLIGEEPRFRIEEKKFLKRLFGG 270

RESULT 9
US-10-767-701-58033
/ Sequence 58033; Application US/10767701
/ Publication No. US20040172684A1
/ GENERAL INFORMATION:
/ APPLICANT: Kovalic, David K.
/ APPLICANT: Zhou, Yihua
/ APPLICANT: Cao, Yongwei
/ TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
/ FILE OF INVENTION: Plants and Uses Thereof for Plant Improvement
/ FILE REFERENCE: 38-21 (5353) B
/ CURRENT APPLICATION NUMBER: US/10/767.701
/ NUMBER OF SEQ ID NOS: 63128
/ SEQ ID NO 58033
/ LENGTH: 174
/ TYPE: PRT
/ ORGANISM: Sorghum bicolor
/ FEATURE:
/ NAME/KEY: unsure
/ LOCATION: (1) (174)
/ OTHER INFORMATION: unsure at all Xaa locations
/ OTHER INFORMATION: Clone ID: 30974845.pcp
/ US-10-767-701-58033
/
Query Match      25.2%; Score 416; DB 16; Length 174;
Best Local Similarity 68.1%; Pred. No. 4.5e-34;
Matches 79; Conservative 13; Mismatches 24; Indels 0; Gaps 0;

QY 51 PELAGETPRIVITSGKGVKTTTANVGLSLARYGFSVAIDADLGRNLDLIGLERN 110
DB 59 PELAGETPRIVITSGKGVKTTTANVGLSLARYGFSVAIDADLGRNLDLIGLERN 118
QY 111 RVNTCEVINGCDRLQALVRDKRNSFELLCSKPSKRLPMGFGKALEWLVDA 166
DB 119 RVHTLADVLAGCDRLQALVRDLQDLHLCLSKPSKRLPLAGSKTLTVVADA 174

RESULT 10
US-10-424-599-219101
/ Sequence 219101; Application US/10424599
/ Publication No. US20040031072A1
/ GENERAL INFORMATION:

```

```

; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 26564
; SEQ ID NO 219101
; LENGTH: 86
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(86)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_39876C.1.pep
; US-10-424-599-219101

Query Match          21.3%; Score 351.5; DB 15; Length 86;
Best Local Similarity 82.8%; Pred. No. 6.3e-28;
Matches 72; Conservative 6; Mismatches 8; Indels 1; Gaps 1;

QY      240 MKGEMMSVLDVQEMLSILGVTPEDSEVIRSTNRGFPVYNKPPTLAGLAFEQAAAR 299
      1 MKKREIILVLDGQKMLGPLGVLPEDSEVIRSTNRGFPVYNKPPTLAGLAFEQTAAR 60
DB      300 LVEODSMKAMVVEEPKRGFSFGG 326
      61 LVEODSMQAVVVEEP-KRGFSFGG 86

RESULT 11
US-10-335-977-9276
; Sequence 9276, Application US/10335977
; Publication No. US20040052799A1
; GENERAL INFORMATION:
; APPLICANT: DOUGLAS SMITH et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES
; RELATING TO HELICOBACTER PYLORI FOR
; DIAGNOSTICS AND THERAPEUTICS
; NUMBER OF SEQUENCES: 10031
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: CD-ROM ISO9660
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: Windows NT 4.0
; SOFTWARE: UNIX
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/335,977
; FILING DATE: 30-Dec-2002
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/993,002
; FILING DATE: 17-Dec-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Mandragouras, Amy E.
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: GTN-018
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7460
; TELEFAX: (617)742-4214
; INFORMATION FOR SEQ ID NO: 9276:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 294 amino acids

```

```

; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHEetical: YES
; ORIGINAL SOURCE:
; ORGANISM: Helicobacter pylori
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (8) LOCATION 1...294
; SEQUENCE DESCRIPTION: SEQ ID NO: 9276:
; US-10-335-977-9276

Query Match          13.5%; Score 224; DB 15; Length 294;
Best Local Similarity 29.1%; Pred. No. 4.6e-14;
Matches 87; Conservative 40; Mismatches 106; Indels 66; Gaps 11;

QY      55 GETPRIVITSGKGVGKTTTANVGLSLARGFVSVAIDALGLRNDLLGLNRYVY 114
      25 GNT-KFIAITSGKGVGKSNISANLAYSLYKKGYGVFADADIGLANDVIGVTKHN- 82
QY      115 TCVEVINGDCRLDQALVNRDKMSNFELLCISKRSLPMG-----FGKALEMLV 164
      83 -ILHALKGEAKLQ-----EITCEIFGLCLFGDSGEILKYSAGALDRV 129
QY      165 DALKTRPEG---SPDFIIDCPAGIDAGFTTAITPANEAVLVTTPDITARDADRVGLL 221
      130 D-----EBCVLSLDYIVIDTGAIGATQAFLNMSDCVIVITTPPSAITDA-----Y 178
QY      222 ECDGIR---DIKATVNV-----RTDMKGDMSVLDVQMLGSLGVLP 265
      179 ACIKINSKNDLFLIANVVAQPKGRATYELFVKAKNIAS-----LELHYGLAE 231
QY      266 EDSEVIRSTNRGFPVYNKPPTLAGLAFEQAAARLVEODSMKAMVVEEPKRGFSFG 324
      232 NSSLKRYVRKRIKRIAPNDLFSOSIDQISLVSKEITGLT-----EIPKGLKSF 266

RESULT 12
US-10-335-977-9277
; Sequence 9277, Application US/10335977
; Publication No. US20040052799A1
; GENERAL INFORMATION:
; APPLICANT: DOUGLAS SMITH et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES
; RELATING TO HELICOBACTER PYLORI FOR
; DIAGNOSTICS AND THERAPEUTICS
; NUMBER OF SEQUENCES: 10031
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: CD-ROM ISO9660
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: Windows NT 4.0
; SOFTWARE: UNIX
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/335,977
; FILING DATE: 30-Dec-2002
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/993,002
; FILING DATE: 17-Dec-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Mandragouras, Amy E.
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: GTN-018
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7460
; TELEFAX: (617)742-4214
; INFORMATION FOR SEQ ID NO: 9277:

```

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; SEQUENCE CHARACTERISTICS:
; LENGTH: 297 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: YES
; ORIGINAL SOURCE:
; ORGANISM: Helicobacter pylori
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (B) LOCATION 1...297
; SEQUENCE DESCRIPTION: SEQ ID NO: 9277:
US-10-335-977-9277

```

```

Query Match      13.5%; Score 224; DB 15; Length 297;
Best Local Similarity 29.1%; Pred. No. 4.7e-14;
Matches 87; Conservative 40; Mismatches 106; Indels 66; Gaps 11;

QY 55 GETPIVITVTSKGGVGTITTTANVGLSLARYGSFVAIDADLGLRNDLLGLENNVY 114
DB 28 GNT-KFAITSGKGGVGSNISANLAYSLKGYVGVFDADIGLANDVIFGVKTKN- 85
QY 115 TCVEYINGDCRLDQALVADKRSNFELLCISKPSKLPWG-----FGKALEMLV 164
DB 86 -IHALKGBAKLQ-----EICEIEPGLCILPGDSGEILKYISGEMALDRFV 132
QY 165 DALKTRPG--SPDFIITDCPAGIDAGFITAITPANEAVLYTTPDITALRDADRVYGL 221
DB 133 D-----EGVLSLDYIYIDTGAGIGATTOAFNLASDCVAVITTPDSATTD-----Y 181
QY 222 ECDGIR-----DIKMYIVRV-----RTDMINGEDMMSVLDVQEMLGSLGVIP 265
DB 182 ACIYINSKNDLEFLINMVAQPKRGATYERLPKVAKNINIA-----LEHLYGAIE 234
QY 266 EDSEVIRSTNGFPLVINKPPTLAGLAFEOAMRWLEQDSKAMVMEEEKRGFTSFF 324
DB 235 NSSILKRYVERKRLRIKRIAPNDLFSSQSIDQASILVSKLETGTL-----EIKPKGLKSF 289

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RESULT 13

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US-10-335-977-7925
; Sequence 7925, Application US/10335977
; Publication No. US20040052799A1
; GENERAL INFORMATION:
; APPLICANT: DOUGLAS SMITH et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES
; RELATING TO HELICOBACTER PYLORI FOR
; DIAGNOSTICS AND THERAPEUTICS
; NUMBER OF SEQUENCES: 10031
; CORRESPONDENCE ADDRESS:
; ADDRESSER: LAHIVE & COCKFIELD
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: CD-ROM ISO9660
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: Windows NT 4.0
; SOFTWARE: UNIX
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/335,977
; FILING DATE: 30-Dec-2002
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/993,002
; FILING DATE: 17-DEC-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Mandragouras, Amy E.
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: GTV-018
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400

```

```

; TELEFAX: (617)742-4214
; INFORMATION FOR SEQ ID NO: 7925:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 368 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: YES
; ORIGINAL SOURCE:
; ORGANISM: Helicobacter pylori
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (B) LOCATION 1...368
; SEQUENCE DESCRIPTION: SEQ ID NO: 7925:
US-10-335-977-7925

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Query Match      12.6%; Score 209; DB 15; Length 368;
Best Local Similarity 24.2%; Pred. No. 2.2e-12;
Matches 80; Conservative 57; Mismatches 112; Indels 82; Gaps 12;

QY 8 STNHQSLLPSSLGKTISSPRFVNNSRRSPIRSVLQFNKPE-----LAGETPR 59
DB 48 SSETTSALIRENISKAMQKGVKALINDIKTP-----KQAPKPTTKNLAKNIKX 98
QY 60 IVVITSGKGVGKTTTANVGLSLARYGSFVAIDADLGLRNDLLGLENNVYTCVEV 119
DB 99 VVMISSGKGVGKSTTSVNLSIALANOKYGLDADVYGPNIPTMNGLO----- 148
QY 120 INGCRLD--QALVDRKRSNFELLCISKPSKLPWG--GKALEMLVDAKTRPE- 172
DB 149 -NADVIMDPGSKKLIIPKAFG-----VSVMWGLLYDSGQSLIMGPMWMAIEQ 197
QY 173 -----GSPDFIITDCPAGIDAGFIT--AITPANEAVLYTTPDITALRDAD----- 216
DB 198 MLDIIMGDDLVLVMDPFGTGAQLTLAQAVPLSAGITVTTQIYSLDARKSLDMFK 257
QY 217 -----VTGLLE-----CDGIRDKMYIVRVRTDMINGEDMMSVLDVQEMLGSLGVIP 266
DB 258 LHPIAGIVENMGSPVCEHCK-----KESEIFGSMMSG--LEAVNQIILAKLPL 306
QY 267 DSEVIRSTNGFPLVINKPPTLAGLAFEOQA 297
DB 307 EPKVRUGDGKDEPIVISHPTVSAKIFEKQA 337

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RESULT 14

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US-10-335-977-7927
; Sequence 7927, Application US/10335977
; Publication No. US20040052799A1
; GENERAL INFORMATION:
; APPLICANT: DOUGLAS SMITH et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES
; RELATING TO HELICOBACTER PYLORI FOR
; DIAGNOSTICS AND THERAPEUTICS
; NUMBER OF SEQUENCES: 10031
; CORRESPONDENCE ADDRESS:
; ADDRESSER: LAHIVE & COCKFIELD
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: CD-ROM ISO9660
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: Windows NT 4.0
; SOFTWARE: UNIX
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/335,977
; FILING DATE: 30-Dec-2002
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/993,002
; FILING DATE: 17-DEC-1997

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 10, 2005, 22:22:13 ; Search time 60 Seconds
(without alignments)
405.593 Million cell updates/sec

Title: US-09-553-431b-2

Perfect score: 1654

Sequence: 1 MASRLRFTNNQSLPLPSL.....KAVVEEPKRGFFSFGG 326

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*

- 1: /cgn2_6/prodata/1/1aa/5A_COMB.pep:*
- 2: /cgn2_6/prodata/1/1aa/5B_COMB.pep:*
- 3: /cgn2_6/prodata/1/1aa/6A_COMB.pep:*
- 4: /cgn2_6/prodata/1/1aa/6B_COMB.pep:*
- 5: /cgn2_6/prodata/1/1aa/6C_COMB.pep:*
- 6: /cgn2_6/prodata/1/1aa/6D_COMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	494	29.9	279	4 US-09-543-681A-4433	Sequence 4433, App
2	483	29.2	274	4 US-09-489-039A-14339	Sequence 14339, A
3	480.5	29.1	273	4 US-09-252-991A-21634	Sequence 21634, A
4	442	26.7	296	4 US-09-328-352-5810	Sequence 5810, App
5	386	23.3	181	4 US-09-540-236-3829	Sequence 3829, App
6	249	15.1	315	4 US-09-252-991A-27725	Sequence 27725, A
7	187.5	11.3	377	4 US-09-252-991A-17627	Sequence 17627, A
8	187.5	11.3	416	4 US-09-328-352-4760	Sequence 4760, App
9	179.5	10.9	364	4 US-09-248-796A-14997	Sequence 14997, A
10	179.5	10.9	399	4 US-09-540-236-2496	Sequence 2496, App
11	177.5	10.7	439	4 US-08-311-731A-1178	Sequence 1178, App
12	168.5	10.2	381	4 US-09-489-039A-8156	Sequence 8156, App
13	164	9.9	267	4 US-09-328-352-7799	Sequence 7799, App
14	163.5	9.9	230	4 US-09-270-767-31308	Sequence 31308, A
15	163	9.9	299	4 US-09-270-767-41683	Sequence 41683, A
16	160.5	9.7	378	4 US-09-543-681A-5534	Sequence 5534, App
17	160	9.7	287	4 US-09-502-540-10550	Sequence 10550, A
18	151.5	9.2	264	4 US-09-107-532A-4581	Sequence 4581, App
19	147.5	8.9	226	4 US-09-583-110-3994	Sequence 3994, App
20	145.5	8.8	258	4 US-09-134-000C-5054	Sequence 5054, App
21	144	8.7	359	4 US-09-134-001C-4842	Sequence 4842, App
22	141	8.5	293	4 US-09-902-540-11166	Sequence 11166, A
23	136.5	8.3	193	4 US-09-107-433-5025	Sequence 5025, App
24	130.5	7.9	221	4 US-09-502-540-10075	Sequence 10075, A
25	130	7.9	241	4 US-09-252-991A-19158	Sequence 19158, A
26	130	7.9	328	4 US-09-538-092-295	Sequence 295, App
27	125	7.6	255	4 US-09-198-452A-860	Sequence 860, App

28	125	7.6	260	4 US-09-438-185A-807	Sequence 807, App
29	122	7.4	280	4 US-09-489-039A-11095	Sequence 11095, A
30	120.5	7.3	267	4 US-09-107-532A-5561	Sequence 5561, App
31	118.5	7.2	236	4 US-09-107-532A-5169	Sequence 5169, App
32	118	7.1	268	4 US-09-134-000C-4636	Sequence 4636, App
33	115.5	7.0	710	4 US-09-902-540-16023	Sequence 16023, A
34	115	7.0	264	4 US-09-540-236-6189	Sequence 6189, App
35	113	6.8	228	4 US-09-328-352-6189	Sequence 6189, App
36	108	6.5	143	4 US-09-248-796A-16948	Sequence 16948, A
37	108	6.5	259	4 US-09-634-238-246	Sequence 246, App
38	108	6.5	293	4 US-09-328-352-4836	Sequence 4836, App
39	107.5	6.5	308	4 US-09-050-739-94	Sequence 94, Appl
40	107.5	6.5	666	4 US-09-050-739-70	Sequence 70, Appl
41	106	6.4	312	4 US-09-252-991A-26439	Sequence 26439, A
42	102.5	6.2	116	4 US-09-621-976-4329	Sequence 4329, App
43	102.5	6.2	204	4 US-09-949-016-11153	Sequence 11153, A
44	101.5	6.1	285	4 US-08-311-731A-34	Sequence 34, Appl
45	101.5	6.1	285	4 US-08-311-731A-36	Sequence 36, Appl

ALIGNMENTS

```
RESULT 1
US-09-543-681A-4433
; Sequence 4433, Application US/09543681A
; Patent No. 6605709
; GENERAL INFORMATION:
; APPLICANT: GARY BRETON
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILIS
; FILE REFERENCE: 2709.1002-001
; CURRENT FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: US/09/543,681A
; PRIOR FILING DATE: 1999-04-09
; NUMBER OF SEQ ID NOS: 8344
; SEQ ID NO 4433
; LENGTH: 279
; TYPE: PRT
; ORGANISM: Proteus mirabilis
; US-09-543-681A-4433

Query Match      29.9%; Score 494; DB 4; Length 279;
Best Local Similarity 40.8%; Pred. No. 2.9e-47;
Matches 116; Conservative 56; Mismatches 80; Indels 32; Gaps 8;

QY 59 RIVITSGKGVGKTTTANVGLSARYGSVAIDADIGLRNLDLLGLNRYVTVE 118
   ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 12 RIVITSGKGVGKTTSSAISTGLAQKHKTVIDFDIGLNLDLIMGCRRVVDVFN 71

QY 119 VINGCDRLDQALVRDRKNSFELLCISKPRSKLPMFGSKALBWLVDALKTRPESGPDIT 178
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 72 VIGDQATLNLQALIKKRTENLYILPASQTRDKDALTRDGE--VEQVDEL---DEMGFDEI 126

QY 179 IIDCPAGIDAGTITATPNEAVLVTPITLRDQRTGLLEC-----DSIRDI 229
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 127 ICDSPGHSGLMLALYFDEALITTNPEVSSVRSDRLGLIAGSRPAKGEDEYKE- 185

QY 230 KAIIVRVRITMDIKGEPMNSVLDOEMTGLSLGLVPEDESVIRSTNRGFPVLNKPPTLA 289
   ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 186 HLLITRYNRGRSRGRMSMEDVLELTCPLIGVPIPEDOSVIRSSNQSGPVLIDSSD-A 244

QY 290 GLAFEQAMRLVEQDSMKAVVVEEP-----KKRGFS-FTGG 326
   ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 245 GRAY-----LDIVNRLIGEHPFRFIEEKKGFLKRLRG 279

RESULT 2
US-09-489-039A-14339
; Sequence 14339, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
```

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; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; PRIOR FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 14339
; LENGTH: 274
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-14339

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```

Query Match
Best Local Similarity 29.2%; Score 483; DB 4; Length 274;
Matches 114; Conservative 57; Mismatches 80; Indels 34; Gaps 8;

QY 59 RIVVITSGKGVGKTTTANVGLSLARYGSVAIADLGLRNLDLGLLENRVNYTCVE 118
DB 7 RIVVITSGKGVGKTTSSAIALGALQKQKTVVIDFDGLNLDLIMGCERRVYDFVN 66
QY 119 VINGDCRLDQALVRDKRMSNFELLCISKRPSKLPNGFCG--KALEMLVDALKTRPEGSPD 176
DB 67 VIGGDATLNGALIKDRRTENLYILPASQTRDKALTRGVKLEEL-----KKMEFD 119
QY 177 FIIDCPAGIDAGFIATITPANEAVALVTPDITADADRVYGLLEC-----DGIRDIK 230
DB 120 FIVCDBPAGIEGALMALYFADEAITTNPEVSVSRDRLIGLASKRSRAENGEBEPK 179
QY 231 --MIVRVRTDMIKGEDMSVLDVQEMGLSLGLVPEDSVIRSTNRGFPVYNKPTL 288
DB 180 EHLLTRVNPVGKGMWLSMEDVLEIRLIMLVGPEIDGVLASNGEFPVILDAASD- 238
QY 288 AGLAEQAAMRLVEDQDSMKAVVEEPP-----KKRGFPFS-FRGG 326
DB 239 AGKAY-----ADTVRLGGERPPRTFEEKKGFLKRLPFG 274

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```

RESULT 3
US-09-252-991A-21634
; Sequence 21634, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 21634
; LENGTH: 273
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-21634

```

```

Query Match
Best Local Similarity 29.1%; Score 480.5; DB 4; Length 273;
Matches 113; Conservative 54; Mismatches 83; Indels 35; Gaps 7;

QY 59 RIVVITSGKGVGKTTTANVGLSLARYGSVAIADLGLRNLDLGLLENRVNYTCVE 118
DB 5 KILVVTSGKGVGKTTSSAIALGALRGFTVIVDPEDGLRDLIMGCERRVYDFVN 64
QY 119 VINGDCRLDQALVRDKRMSNFELLCISKRPSKLPNGFCGKALEMLVDAL-----KTRPE 172
DB 65 VVNGEATLTQALIDKXLENLHVLAASQTRDK-----DALTKGVEKVAWE 110

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QY 173 GSPDF--FIIDCPAGIDAGFIATITPANEAVALVTPDITADADRVYGLLECDDGIRDIK 230
DB 111 LRKDFEYIICDSPAGIEGALMALYFADEAITTNPEVSVSRDRLIGLASKRSRAENGEBEPK 170
QY 231 -----MIVRVRTDMIKGEDMSVLDVQEMGLSLGLVPEDSVIRSTNRGFPVYNKPTL 288
DB 171 GEPKIEHLLTTRVNPVGKGMWLSMEDVLEIRLIMLVGPEIDGVLASNGEFPVILDAASD- 238
QY 283 NKPEPTLAGLAFEQAAMRLVEDQDSMKAVVEEPPKRGFPFS-FRGG 326
DB 231 DEQSD-AGQAYSDAVDRILGKEIPHRFL---DVQKGFQRLPFG 271

```

```

RESULT 4
US-09-328-352-5810
; Sequence 5810, Application US/09328352
; Patent No. 6562988
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
; FILE REFERENCE: GTC99-039A
; CURRENT APPLICATION NUMBER: US/09/328,352
; PRIOR FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 8252
; SEQ ID NO 5810
; LENGTH: 296
; TYPE: PRT
; ORGANISM: Acinetobacter baumannii
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: (251)
; OTHER INFORMATION: Identity of amino acid sequences at the above locations are unk.
US-09-328-352-5810

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```

Query Match
Best Local Similarity 26.7%; Score 442; DB 4; Length 296;
Matches 102; Conservative 53; Mismatches 84; Indels 16; Gaps 5;

QY 59 RIVVITSGKGVGKTTTANVGLSLARYGSVAIADLGLRNLDLGLLENRVNYTCVE 118
DB 29 KIVVITSGKGVGKTTSSAIALGALRGFTVIVDPEDGLRDLIMGCERRVYDFVN 88
QY 119 VINGDCRLDQALVRDKRMSNFELLCISKRPSKLPNGFCGKALEMLVDALKTRPEGSPDFI 178
DB 89 VINNEARLQDALIRDKDLENLYILPASQTRDKALSDGVAR--VIDELSQ-----EFDYI 142
QY 179 FIIDCPAGIDAGFIATITPANEAVALVTPDITADADRVYGLLEC-----DGIRDIK 230
DB 143 ICDSPAGIEGALMALYFADEAITTNPEVSVSRDRLIGLASKRSRAENGEBEPK 170
QY 231 MIVRVRTDMIKGEDMSVLDV--QEMGLSLGLVPEDSVIRSTNRGFPVYNKPTL 289
DB 203 LCITRFNFERADRGEMLTIDDISKIDILRVPTLGVIPCESVLOASNEGFPVILYS-ETIA 261
QY 290 GLAEQAAMRLVED 304
DB 262 GQAYDVLVARFLGED 276

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RESULT 5
US-09-540-236-3829
; Sequence 3829, Application US/09540236
; Patent No. 6673910
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO MORAXELLA CATAR
; FILE REFERENCE: 2709.2005-001
; CURRENT APPLICATION NUMBER: US/09/540,236
; PRIOR FILING DATE: 2000-04-04
; NUMBER OF SEQ ID NOS: 3840

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; SEQ ID NO 3829
; LENGTH: 181
; TYPE: PRT
; ORGANISM: M.catarhalis
US-09-540-236-3829

```

Query Match	23.3%	Score	386	DB	4	Length	181
Best Local Similarity	48.8%	Pred. NO.	2.5e-35				
Matches	81	Conservative	36	Mismatches	41	Indels	8
						Gaps	2

Dy 59 RIVVITSGKGVGKTTTANGSLARXGFVSVAIDADLGELNLDLLGLBKRVNYTCVE 118
:::|:|||||||::|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:
Db 18 KIVAVTSGKGVGKTTSASFGAGLAKRGFKTVIIDPDVGRLDLMGCENRIVYDFVD 77

```

09  VINGCRDLDALVRDRMWSNELLCTSKPRKCPMGEG--KALEWLDALKRPESSPD 166
    ||:::|||||:::|:::|:::|:::|:::|:::|
78  VISGNAKLAQALVKQKQFENLYILPISQTRDALTDEGVAKYMKELADDMKF-----D 131
Db

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177 FIIIDCPAGIDAGFIITAIIPANEAVLVIPIIDIAIKDADRIGLLE 222
132 FTICDSPAGIERGAQLAMVYHADEALIVTNPEVSSVRDSDRIIGILQ 177

```

RESULT 6
US-09-252-991A-27725
: Sequence 27725, Application US/09252991A
: Patent No. 6551795
: GENERAL INFORMATION:
: APPLICANT: Marc J. Rubenfield et al.
: TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
: TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
: FILE REFERENCE: 107196.136
: CURRENT APPLICATION NUMBER: US/09/252,991A
: PRIOR FILING DATE: 1999-02-18
: PRIOR APPLICATION NUMBER: US 60/074,788
: PRIOR FILING DATE: 1998-02-18
: PRIOR APPLICATION NUMBER: US 60/094,190
: PRIOR FILING DATE: 1998-07-27
: NUMBER OF SEQ ID NOS: 33142
: SEQ ID NO 27725
: LENGTH: 315
: TYPE: PRF
: ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-27725

```

Query Match	15.1%	Score 249	DB 4	Length 315
Best Local Similarity	27.1%	Pred. No. 26-19		
Matches	80	Conservative	46	Mismatches 101
			Indels	68
			Gaps	9
QY	59	RIVVITSGKGVGKTTTANVGLSLARQGSVAVIDADIGLRNLDLLENRVNTCYE	118	
DB	46	QVIAATGKGGKGGKKNVSNLALADLGRRWLLDADLGLNVDVLLGLTRK--RTLAD	103	
QY	119	VINGDCRRDQALVDRKWSNFELLCISKRSKLPMGFGSKALEWLDAKTRPEGSP--	175	
DB	104	VIEEGCEL-----RDVLLGPGGVRLVPAASGTQSNVHLSPQH	142	
QY	176	-----DFIIIDCPAGIDAGETITTAITPANEAVLVUTTPDITLRLDRDRTGILL	221	
DB	143	AGLIDAFSDISDNLDVLVDTAAGIGDSVSVFRAQEVLLAVCDPEPSTITAYALIKLL	202	
QY	222	ECD-GIRDIKMIIVNRVTDMIKGEIMMS-----VLDDQEMLGSLIGVIPEDSEVIR	272	
DB	203	NRDHQMTFRVLVANNANHSRQ-EGRNILFALTLTKVTDRFLDV-----ALQYVGVIPIYDESVRK	257	
QY	273	STNRGFRVLVKNRPRLTAGLAFQDAAMRLVEDQSMKAMVVEER---KKRGFSFF	324	
DB	258	AVQKRAVYEAEPKRSKASLAFKAVNOK-----VDSWFLPAMPNGHLEFF	301	

RESULT 7
US-09-252-991A-17627
; Sequence 17627, Application US/09252991A

```

: Patent No. 6551795
: GENERAL INFORMATION:
: APPLICANT: Marc J. Rubenfield et al.
: TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
: TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
: FILE REFERENCE: 107196.136
: CURRENT APPLICATION NUMBER: US/09/252.991A
: CURRENT FILING DATE: 1999-02-18
: PRIOR APPLICATION NUMBER: US 60/074,788
: PRIOR FILING DATE: 1998-02-18
: PRIOR APPLICATION NUMBER: US 60/094,190
: PRIOR FILING DATE: 1998-07-27
: NUMBER OF SEQ ID NOS: 33142
: SEQ ID NO 17627
: LENGTH: 377
: TYPE: PRT
: ORGANISM: Pseudomonas aeruginosa
: US-09-252-991A-17627

```

Query Match	11.3%	Score 187.5	DB 4	Length 377
Best Local Similarity	25.9%	Pred. No. 2.5e-12		
Matches 70	Conservative 43	Mismatches 110	Indels 47	Gaps 9

Oy 52 ELAEETPRIVVITSKGVGKTTTANVGSLARQFSVAVIDADGLRNDLTLLEENR 111
↑ :
Db 106 EVMGNVKNIIVAVASRGVSKSTTMNLALALARREGARVGLDADIYGPSQGIMFGLPEG 165

QY 112 VNVTCEVINGDCRRDQALVRDKIRKSNFELLCISKRKSLPMGF--GKALEW-----162
 : : : : : : : : : : : :
 Db 166 T-----RPRKREQKV--FEPL-EAHGVQVMSMAFLTDDSTPVVWRGPMVS 207

163 -LVAVAKNRKFGSGDFEVLVLLFGLFNGSDVGLTAT -FEMVLLVLLFGLFNGSDVGLTATNDKNA -
208 GALLQTLITQATAMNDPDYLVVDMFPGGDIQTLTAQKRVAGAVITVTPQDILLDAKGV 267

268 EMFRKVPVLGVENMAVH--ICSNCHAEHLFEGGEGEKLAAQ--FGVELLAMP LS 322

323 IAIRQADSGRPVIADPESQAMLQEIA 352

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RESULT 8
US-09-328-352-4760
; Sequence 4760, Application US/09328352
; Patent No. 6562958
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
; TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: GTC99-03PA
; CURRENT APPLICATION NUMBER: US/09/328,352
; CURRENT FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 8252
; SEQ ID NO 4760
; LENGTH: 416
; TYPE: PR1
; ORGANISM: Acinetobacter baumannii
US-09-328-352-4760

```

Query Match	11.3%	Score 187.5;	DB 4;	Length 416;
Best Local Similarity	23.7%	Pred No. 2.9e-12;		
Matches	73;	Conservative	117;	Indels 67; Gaps 10

QY 33 NNPSRRSPRLSLCPNRRKPELAGEHPRIWITTSKGGVGKRTTANGLSLRYSFVSVA 92
Db 137 NNP-----PQGAAPQQRDVFLHPRIRKIVLVSSGKGSGVSKSTTTVMALALQKMGKLGCV 192

QY 1ADADGGRNIDDELG-----LENNKNYICEV-----INGLCRLDDALVRKRM 136

Db 193 LDADLYGSPSPTMLGNAGKTPRIESENFPVPLDAYGMAVLISGHLTG----- 239

```

QY 137 SNFELLSKPSKLPKMF-GKALEWLVDAKTRPGSPDFIICCPAGIDAGFTTA- 194
Db 240 -----NNTPVAMRGPBKATGALMOLFNOGLTWLPDIDVLMIDMPETGSIQTLAQ 287
QY 195 -TPANEAVLTPPTDITALLRDADRVTLGECGIRDIKIMVNRRTDM-----I 241
Db 288 RLPVTSIIITTPQNVALLDRTKGIELFNKVGI-PVLGVENNSTHICSNCGHEEQIFGI 346
QY 242 KGEPMMSVLDOVQEMLSLGLVIRPEDESEVIRSTRNGEPVLANKPPTL-AGLAFEOQAWRL 300
Db 347 GGGDKLS-----EYHIFLGLRPLNQLIREHADQCKPSVYIAMDADSYIDIAKAWMO 401
QY 301 VEQDSMKA 308
Db 402 IERVFORA 409

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RESULT 9
US-09-248-796A-14997
; Sequence 14997, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstein et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
; FILE REFERENCE: FOR DIAGNOSTICS AND THERAPEUTICS
; CURRENT APPLICATION NUMBER: US/09/248,796A
; PRIOR FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 14997
; LENGTH: 364
; TYPE: PRT
; ORGANISM: Candida albicans
US-09-248-796A-14997

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Query Match 10.9%; Score 179.5; DB 4; Length 364;
Best Local Similarity 24.4%; Pred. No. 1.9e-11;
Matches 73; Conservative 40; Mismatches 103; Indels 83; Gaps 11;
QY 52 ELAGEYTR-----IVVITSGKGVGKTTTANVGLSLARYGFSVAIDADLGLRNDL 104
Db 74 ELLOEVFKSIEHVKHILLISGKGVKSSTVTTQVALTLVKNKGFVNGVLDLDTGSPSLPR 133
QY 105 LLLGLENNV-----NTCYEVINGDCRLDQALVRDKRMSNFELICISKPSKLPKMFSGK 158
Db 134 MFEVENKQVHQSTRGWVPVSVNNNNNOG---TDSKGNLSLMSLG-----FLIGDRGN 184
QY 159 ALFW-----LVDAKTRPGSPDFIICCPAGIDAGFTTA-----ITPANEA 200
Db 185 SVVWRGPKTKAMIKQFLKDVWVWSAFTPLDYLITPPTGSDHEIALAEELRWANPIDIKA 244
QY 201 VLVTPDITALLDADR-----VTGLLE-----CDGIRDIKIMVNRVATWIKG 243
Db 245 IIVTTPQVATADVREINFCCKVNFQILGIVENNSGFCICHGECNINITS-----GG 298
QY 244 EDMMSVLDOVQEMLSLGLVIRPEDESEVIRSTRNGEPVLANKPPTLAGLAFEOQAWRLVE 302
Db 299 GKALS-----EQNLNLTIVGNVPIDPQVE-----LVLELQNEKENKLLIE 337

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RESULT 10
US-09-540-236-2496
; Sequence 2496, Application US/09540236
; Patent No. 6673910
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO MORAXELLA CATAR
; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS

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; FILE REFERENCE: 2709.2005-001
; CURRENT APPLICATION NUMBER: US/09/540,236
; CURRENT FILING DATE: 2000-04-04
; NUMBER OF SEQ ID NOS: 3840
; SEQ ID NO 2496
; LENGTH: 399
; TYPE: PRT
; ORGANISM: M.cattarrhalis
US-09-540-236-2496

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Query Match 10.9%; Score 179.5; DB 4; Length 399;
Best Local Similarity 25.9%; Pred. No. 2.2e-11;
Matches 74; Conservative 48; Mismatches 125; Indels 39; Gaps 11;
QY 9 TTHQSILPSSLSOKTLISSPRFVNPPERSPIRSVLQFNKKPLAGETPRIVITSGKG 68
Db 99 TTQPNLVKTHHTPKTTDAISAQHDKPPTXATNQ-SQLNANPRT-----HIIAVSGKG 153
QY 69 GVGKTTTANVGLSLARYGFSVAIDADLGLRNDLGLLENRVNVCVEVINGDCRLDQ 128
Db 154 GVGKSTTVNIALALQKMGKRVGILDADIVGSPSIPMLGVA-----TKRIVEN-----DQ 204
QY 129 ALVRDKRMSNFELICISK--PSKLPKMFSG-KALEWLVDAKTRPGSPDFIICCPAG 185
Db 205 FIPIDA--NGMAVLSIGNLDAENTPIAMRGIKATGALMOLVYQTNWPPOLDYLLIMPPG 262
QY 186 IDAGFTTA--TPANEAVLTPPTDITALLRDADRVTLGECGIRDIKIMVNRV----- 236
Db 263 TGDQLTLACRIPLTGAIIYVTPQHALDRAKKGVEFHKTRIDIRVGLIENNALHTCTHC 322
QY 237 -RTDM-----KGEPMMSVLDOVQEMLSLGLVIRPEDESEVIRSTRNG 277
Db 323 GHTAIFRTGGGDEMAYADV-----PLIGQLFDASTIRVAMDNQ 362

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RESULT 11
US-08-311-731A-178
; Sequence 178, Application US/08311731A
; Patent No. 6583266
; GENERAL INFORMATION:
; APPLICANT: SMITH, DOUGLAS
; APPLICANT: MAO, JEN-I
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES
; TITLE OF INVENTION: RELATING TO MYCOBACTERIUM TUBERCULOSIS AND LAPRAE FOR
; NUMBER OF SEQUENCES: 411
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: WOLF, GREENFIELD & SACKS, P.C.
; STREET: 600 ATLANTIC AVENUE
; CITY: BOSTON
; STATE: MASSACHUSETTS
; COUNTRY: USA
; ZIP: 02210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/311,731A
; FILING DATE:
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: GATES, EDWARD R.
; REGISTRATION NUMBER: 31,616
; REFERENCE/DOCKET NUMBER: C0044/7125
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/720-3500
; TELEFAX: 617/720-2441
; INFORMATION FOR SEQ ID NO: 178:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 439 amino acids
; type: amino acid

```

TOPOLOGY: linear
 MOLECULE TYPE: protein
 HYPOTHETICAL: YES
 ORIGINAL SOURCE:
 ORGANISM: Mycobacterium leprae
 US-08-311-731A-178

Query Match 10.7%; Score 177.5; DB 4; Length 439;
 Best Local Similarity 24.3%; Pred. No. 4.3e-11;
 Matches 76; Conservative 60; Mismatches 134; Indels 43; Gaps 12;

QY 32 VNNPERRSPDIRSVLOFN-RKPELAGETP---RIVVITSGKGVGKTTTANVGLSLARY 86
 DB 144 VMSDEQRTLRKRLRGDAEPMIPFAQPNLSLRVTVASGKGVGKSTVTNLAIAAR 203
 QY 87 GRSVAIDADLGLRNLDLGLLENRYNYCVCEVINDCDLQALVADKMSPELLCISK 146
 DB 204 GLAVGLDADIHGHSIPRMWGSNQR-----PIQESMLPPIVHE-----VKVISIQ 251
 QY 147 -PRSKLPWGGGKAL-----EWLVDAKTRPESGSPFIIDCPAGID--AGFITATTPAN 198
 DB 252 FTEGNTPVWRGEMLRALQGFISDVR---WGDLVLMLDLPPGCGDIAISVAQLIPNA 307
 QY 199 EAVLVTPDITALRDADRYTGLLECDGIRDIKMIVNRVETDMIKGEDMMSVL-----DV 252
 DB 308 EILVVTTPQLAAAEVAER-AGSIALQTRQIRIGVENMGSLMMPDGSRLQVFGEGGQGV 366
 QY 253 QEMLG-----ISLGVIPEDSEVIRSTNRGFPVLVINKPPTLAGLAFEOAMRL-VEQDS 305
 DB 367 ARSLRAVGTDVPLDQLDPLDPAVAGSGIPVIVNASDSPVKELRIADGLSSRRQR 426
 QY 306 MKAVVVEEPPKKR 318
 DB 427 LAGVSLGLDPSRR 439

RESULT 12

US-09-489-039A-8156
 Sequence 8156, Application US/09489039A
 Patent No. 6610836
 GENERAL INFORMATION:
 APPLICANT: Gary Breton et. al
 TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
 TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
 FILE REFERENCE: 2709.2004001
 CURRENT APPLICATION NUMBER: US/09/489,039A
 CURRENT FILING DATE: 2000-01-27
 PRIOR APPLICATION NUMBER: US 60/117,747
 PRIOR FILING DATE: 1999-01-29
 NUMBER OF SEQ ID NOS: 14342
 SEQ ID NO 8156
 LENGTH: 381
 TYPE: PRT
 ORGANISM: Klebsiella pneumoniae
 US-09-489-039A-8156

Query Match 10.2%; Score 168.5; DB 4; Length 381;
 Best Local Similarity 24.3%; Pred. No. 3.6e-10;
 Matches 74; Conservative 42; Mismatches 105; Indels 83; Gaps 11;

QY 41 TSVLOFNKRPKELAGTPRIVVITSGKGVGKTTTANVGLSLARYGFSVAIDADLGR 100
 DB 103 IATLKVKKQOPVNG-VKNITAISSGKGVGKSTVNNLALAAAGAKYGIIDDIYGP 161
 QY 101 NLDLGLG-----NRVNTCVCEVINDCDLQALVADKMSPELLCISK 138
 DB 162 SIPTMGAEDSRPTSDGTHMARIKYLATNSIGLVND-----DNAMV-----WR- 208
 QY 139 FELLCTSKRPSKLPWGGGKALEWLVDAKTRPESGSPFIIDCPAGIDAGFTAI--TP 196
 DB 209 -----GPMATKALMQMQLTLPDLDVLMPPGTGDIQITLQANIP 251
 QY 197 ANEAVLVTPDITALADADR-----VTGLLECGDIRDKMIV--NRVETDMIKG 243

DB 252 VTGAVVVTPQDIALIDAKKGIWEDKXEMPVLIGLE-----NMSNHCISNGHHPITFG 306
 QY 244 EDMMSVLVQEWLGLSLGIVIPEDSEVIRSTNRGFPVLVINKPPT-----LAGLAFRQ 295
 DB 307 AG-GAQKLAEXYHTQLGQWPLHITREDLDNGTPTVVARPDSEPTDIYROLAQRVAQ 364
 QY 296 AAMR 299
 DB 365 MYWQ 368

RESULT 13

US-09-328-352-7799
 Sequence 7799, Application US/09328352
 Patent No. 6562958
 GENERAL INFORMATION:
 APPLICANT: Gary L. Breton et al.
 TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
 TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
 FILE REFERENCE: GTC99-03PA
 CURRENT APPLICATION NUMBER: US/09/328,352
 CURRENT FILING DATE: 1999-06-04
 NUMBER OF SEQ ID NOS: 8252
 SEQ ID NO 7799
 LENGTH: 267
 TYPE: PRT
 ORGANISM: Acinetobacter baumannii
 US-09-328-352-7799

Query Match 9.9%; Score 164; DB 4; Length 267;
 Best Local Similarity 21.2%; Pred. No. 6.6e-10;
 Matches 62; Conservative 62; Mismatches 100; Indels 68; Gaps 10;

QY 59 RIVVITSGKGVGKTTTANVGLSLARYGFSVAIDAD-----LGRNLDLIGLEN 110
 DB 10 QIIAIANQKGVGKTTTAVNLAASLAVLKKRVLVDIDQGNATMGSGIQKNDLL-----64
 QY 111 RNNYCVCEVINDCDLQALVADKMSPELLCISKPRSKLPWGG-KGALEWLVDAKLT 169
 DB 65 ---YSTVDLGEVPLETHI--OKAEVGYKVLGSNLSGVELAJAEQGREFTLNALN 119
 QY 170 RPEGSPDFIIDCPAGIDAGFTAITPANEAVLVTPDITALRDADRYTGLLEC-----D 224
 DB 120 EIRDSFDYIIVCABSLS-----LIT--VNLAANDGVLIIPQCEVYALE 162
 QY 225 GIRDIMIVNRVETDMIKGEDMMSVL-----DVQEMLGSLIG-VIPED 267
 DB 163 GLADLTORTIDRIOKALNPDLFEIIGVLRITWYDARNALTRDVSALAEQYFGKLVDTVIFPN 222
 QY 268 SEVIRSTNRGFPVLVINKPPTLAGLAFEOAMRLVEDSKKAVVVEEPPKKR 319
 DB 223 VRLAEPAHGLPVY-----FEKSSGAVAYVNLAAEMLKSKVKKG 264

RESULT 14

US-09-270-767-33308
 Sequence 33308, Application US/09270767
 Patent No. 6703491
 GENERAL INFORMATION:
 APPLICANT: Homburger et al.
 TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
 FILE REFERENCE: File Reference: 7326-094
 CURRENT APPLICATION NUMBER: US/09/270,767
 CURRENT FILING DATE: 1999-03-17
 NUMBER OF SEQ ID NOS: 62517
 SOFTWARE: Patentin Ver. 2.0
 SEQ ID NO 33308
 LENGTH: 230
 TYPE: PRT
 ORGANISM: Drosophila melanogaster
 US-09-270-767-33308

Query Match
Best Local Similarity 9.9%; Score 163.5; DB 4; Length 230;
Matches 58; Conservative 29; Mismatches 83; Indels 45; Gaps 6;
QY 42 RSVLOPNRKPELAGETPRIVITSGGKVTITANVGLSLARYGSVAIDADLGLRN 101
DB 6 RRMKLLNRFIML-DVKKNVIVVLSGGGKSTVSTQSLARKMGFKVGLDIDLCPS 64
QY 102 LDLLGLENNRYNYTCVEVINGDCRLDQALVRDKRW-----SNFELLCISKPRSKLPMGF- 155
DB 65 VPYLGLEGRDIFQC-----DDGWVYVYTBESQTLAV-----MSIGPL 102
QY 156 -----GKALEMLVDALKTRPESGDPFIIDCPAGIDAGFIYAITPANE----- 199
DB 103 LKNREDPVIMRGPKTMMIRQFLDVAMDELDYLIIDTPPGTSDEHITYMECLKEVGCHG 162
QY 200 AVLTTPDITALPRADRVGTGLECDGIRDKIMVN 234
DB 163 AIVTTPQVALTDVRKEITFCCKTGINILGIVEN 197

RESULT 15
US-09-270-767-41683
; Sequence 41683, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 41683
; LENGTH: 299
; TYPE: prt
; ORGANISM: Drosophila melanogaster
US-09-270-767-41683

Query Match 9.9%; Score 163; DB 4; Length 299;
Best Local Similarity 22.7%; Pred. No. 1e-09;
Matches 65; Conservative 34; Mismatches 95; Indels 92; Gaps 9;
QY 60 IVVITSGKGVGKTTTANVGLSLARYGSVAIDADLGLRNLDLLGLENNRYNYTCVEV 119
DB 47 IIVVASKGVGKSTVAVNFACSLAKLGRVGLDGDIFGPTIPLIMNVHG----- 97
QY 120 INGBCRDQALVRDKRW-----SNFELLCISKPRSKLPMGF- 171
DB 98 -----EPVVDKMLMPPQNYNVKCLSMGMLTPVETSYIMRGPLVMSAIQRLLKGTD 149
QY 172 EGSBDFIIDCPAGI-DAGF-ITAITPANEAVLYTTPDITALRDADRYTGLLECDGIRDI 229
DB 150 WGLLDVLYIDTPGTGDVHLSQHAFIGVILVTTPHRAV-----QVT----- 194
QY 230 KMIIVNRRTDMTIGEDPMGSLVQEMLSLGLVY----- 264
DB 195 -----LKGASM-----YEKLVNPIFGVVENMKYITCONCQRLFFPKDSRISS 237
QY 265 -----PEDESVIRSTNRGPFVLYNRPPTLAGIAPQAMRLVE 302
DB 238 LPRKLSLPLDSRIADSNESGVVYIKYPRDSKYSGLFTQLAEITQ 283

Search completed: March 10, 2005, 23:49:14
Job time : 61 secs

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OM nucleic - nucleic search, using sw model

Run on: March 10, 2005, 18:03:37 ; Search time 210 Seconds
(without alignments)
7620.374 Million cell updates/sec

Title: US-09-553-431B-1

Perfect score: 978
Sequence: 1 atgcgcctctctgagatgtt.....tctctcttcttgcgcgc 978

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database : Issued Patents NA:
1: /cgn2_6/prodata/1/ina/5A.COMB.seq:*
2: /cgn2_6/prodata/1/ina/5B.COMB.seq:*
3: /cgn2_6/prodata/1/ina/5A.COMB.seq:*
4: /cgn2_6/prodata/1/ina/6B.COMB.seq:*
5: /cgn2_6/prodata/1/ina/PCTUS.COMB.seq:*
6: /cgn2_6/prodata/1/ina/backfillseq1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	88.4	9.0	546	US-09-540-236-1909	Sequence 1909, Ap
2	87.2	8.9	891	US-09-328-352-1684	Sequence 1684, Ap
3	86.4	8.8	840	US-09-543-681A-261	Sequence 261, App
4	85.2	8.7	825	US-09-489-039A-7168	Sequence 7168, Ap
5	79.8	8.2	822	US-09-252-991A-5063	Sequence 5063, Ap
6	79.8	8.2	903	US-09-252-991A-5154	Sequence 5154, Ap
7	73	7.5	31940	US-09-596-002-13	Sequence 13, Appl
8	65	6.6	640681	US-09-790-988-1	Sequence 1, Appl
9	50.6	5.2	1664976	US-08-916-421B-1	Sequence 1, Appl
10	50.6	5.2	1664976	US-08-692-570-1	Sequence 1, Appl
11	46.6	4.8	7218	US-08-232-463-14	Sequence 14, Appl
12	42.6	4.4	648	US-09-252-991A-1129	Sequence 1129, Ap
13	42.6	4.4	1134	US-09-252-991A-1056	Sequence 1056, Ap
14	42.6	4.4	1254	US-09-252-991A-904	Sequence 904, App
15	42	4.3	2793	US-09-231-017B-1015	Sequence 1015, Ap
16	40.8	4.2	17726	US-09-902-540-1148	Sequence 1148, Ap
17	40.4	4.1	2460	US-09-328-352-524	Sequence 524, App
18	40.2	4.1	601	US-09-949-016-77656	Sequence 77656, A
19	40.2	4.1	105055	US-09-949-016-14001	Sequence 14001, A
20	40	4.1	14700	US-09-949-016-14979	Sequence 14979, A
21	39.8	4.1	648	US-09-252-991A-10965	Sequence 10965, A
22	39.8	4.1	948	US-09-252-991A-11154	Sequence 11154, A
23	39.8	4.1	2073	US-09-252-991A-11096	Sequence 11096, A
24	39	4.0	1107	US-08-991-300-1	Sequence 1, Appl
25	38.6	3.9	582	US-09-107-433-2422	Sequence 2422, Ap
26	38.6	3.9	681	US-09-583-110-1333	Sequence 1333, Ap
27	38.4	3.9	1664976	US-08-916-421B-1	Sequence 1, Appl

C	28	38.4	3.9	1664976	4	US-09-692-570-1	Sequence 1, Appl
C	29	35.8	3.7	601	4	US-09-949-016-165983	Sequence 165983, A
C	30	35.8	3.7	6161	4	US-09-949-016-16419	Sequence 16419, A
C	31	35.6	3.6	6659	4	US-09-321-987B-1	Sequence 1, Appl
C	32	35.4	3.6	1287	3	US-09-461-474-1	Sequence 1, Appl
C	33	35	3.6	1590	3	US-08-887-534A-73	Sequence 73, Appl
C	34	35	3.6	1590	4	US-09-527-431-73	Sequence 73, Appl
C	35	3.6	1590	4	US-09-446-861-73	Sequence 73, Appl	
C	36	3.6	7778	4	US-08-956-171E-48	Sequence 48, Appl	
C	37	3.6	7778	4	US-08-781-986A-48	Sequence 48, Appl	
C	38	34.8	3.6	453	4	US-09-270-767-8770	Sequence 8770, Ap
C	39	34.8	3.6	453	4	US-09-270-767-24052	Sequence 24052, A
C	40	34.8	3.6	1146	4	US-09-489-039A-985	Sequence 985, App
C	41	34.6	3.5	536165	4	US-09-214-808-1	Sequence 1, Appl
C	42	34.4	3.5	11978	4	US-09-792-568-8	Sequence 8, Appl
C	43	34.4	3.5	12438	4	US-09-792-568-9	Sequence 9, Appl
C	44	34.2	3.5	1806	4	US-09-248-796A-184	Sequence 184, App
C	45	34	3.5	431	4	US-09-497-491-30	Sequence 30, Appl

ALIGNMENTS

RESULT 1
US-09-540-236-1909
; Sequence 1909, Application US/09540236
; Patent No. 6673910
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO MORAXELLA CAT. A.
; FILE REFERENCE: 2709.2005-001
; CURRENT APPLICATION NUMBER: US/09/540,236
; NUMBER OF SEQ ID NOS: 3840
; SEQ ID NO 1909
; LENGTH: 546
; TYPE: DNA
; ORGANISM: M catarrhalis
US-09-540-236-1909

Query Match 9.0%; Score 88.4; DB 4; Length 546;
Best Local Similarity 50.6%; Pred. No. 3.2e-19;
Matches 249; Conservative 0; Mismatches 231; Indels 12; Gaps 1;

QY	178	ATGCTGTTATCACTTCGGAAGGCGGTGGTGAAGACGACCAACCGCAATGTC	237
DB	55	ATGCTGTAGTAACTTCAGTAAGGCGGTGCGCAAAACCAACCACTGCATCATTT	114
QY	238	GGTCTCTCTGCTGCTGTTACGTTCTCAGTTGCGCCATTGACGCCGACTTGTC	297
DB	115	GGTCAAGGGGTGCTCAAGCGTGCCTTAAACGATCATCTTATGATTCGGTTG	174
QY	298	CGTAACCTGCATCTCCTCCTAGGTTAGAGATCGATCAATTACCTTCGTCAGGTT	357
DB	175	CGTAATTGATCTTATTTAGGTTGGAAGATCGATGCTGATGATGATG	234
QY	358	ATTAACGAGATGTCGTCGATCAAGCTCGTACGATGAAGCGTTCGATTC	417
DB	235	ATCAGTGTATCCCAAGCTTCTCAAGCTTGTACGACCAACCAATTGAAATCTA	294
QY	418	GAATTCATATGATATCTTAACCTAGTCAAACTTCGATGGGATTTGGTGAAGCA	477
DB	295	TACATTTTGCCTGATCGCAAGACGACAAAGAGCTTCGACGATGAAGCGTGGCT	354
QY	478	TTGAATGCGCTTGATGATGCTTGAAGATGACCGAAGGTTACCGGATTTTCATCATC	537
DB	355	AAAGTCATGAAGAGCTGGC-----AGATGATATGAATTTGATTTTATCATT	402
QY	538	ATGATGTTCTTCGAGAAATGATGCGGATTTATACCGCATTTACTCGGCGAATGA	597
DB	403	TGTGACAGCCCTCGGGGTATTTAGCGTGTGACACAGCTTCGATGATCATGCTGATGA	462

Qy	598	GCAGTCTCGTAA	CACTCCGATAT	TAACAGCGTTA	AGGATGCGA	AGAGGTTACGGT	657
	463	GCAC	TATCGTTACCA	TCTCAGATTC	CATCGGTAC	CAACTGATCATTTGGT	522
Qy	658	TTGTTA	GAAATGC	669			
	523	ATTC	TACAAAGC	534			
Db							

RESULT 2

```

US-09-328-352-1684
Sequence 1684, Application US/09328352
Patent No. 6562958
GENERAL INFORMATION:
APPLICANT: Gary L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
FILE REFERENCE: BAUWMANNI FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT APPLICATION NUMBER: US/09/328-03PA
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
SEQ ID NO 1684
LENGTH: 891
TYPE: DNA
ORGANISM: Acinetobacter baumannii
FEATURE:
NAME/KEY: unsure
LOCATION: (751)
OTHER INFORMATION: Identity of nucleotide sequences at the above locations are unkn
US-09-328-352-1684

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US-09-543-681A-261
; Sequence 261, Application US/09543681A
; Patent No. 6605709
; GENERAL INFORMATION:
; APPLICANT: GARY BRETON
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILIS
; FILE REFERENCE: 2709,1002-001
; CURRENT APPLICATION NUMBER: US/09/543,681A
; CURRENT FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: US 60/128,706
; PRIOR FILING DATE: 1999-04-09
; NUMBER OF SEQ ID NOS: 8344
; SEQ ID NO 261
; LENGTH: 840
; TYPE: DNA
; ORGANISM: Proteus mirabilis
US-09-543-681A-261

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US-09-489-039A-7168
; Sequence 7168, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; FILE REFERENCE: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US/09/489,039A
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 7168
; LENGTH: 825
; TYPE: DNA
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-7168

Query Match
Best Local Similarity 8.7%; Score 85.2; DB 4; Length 825;
Matches 248; Conservative 0; Mismatches 213; Indels 15; Gaps 2;

QY 169 ACGCCGCGATCGTGTATCACTCCGGAAGAGCGGTGTGAAGAAGCAACACACC 228
DB 13 ATGGACCGATATATTGTGTGACTTCGGGTAAAGGGGGCGTTGGCAAGACACCTCCAGC 72

QY 229 GCAAAATGTCGTCTCTCTCTCGCTGTTACGGTTTCTCAGTTGTGCCATTACGCCGAC 288
DB 73 GCGGCGATCGCTACAGGTTTGCCCAAGAGGAGAAACCGTGTATCGACTTTCGAC 132

QY 289 CTGTGTCCTCGTAACCTCGATCCCTCAGGGTTAGAGATCGATCAATTACCTTGC 348
DB 133 ATCGGCTGCGTAACCTCGATCTGATTTAGGCTGGAACGTCGCTGTTATGATTTTC 192

QY 349 GTCGAGTTATTAACGAGATTGCTCTCGATCAAGCTCTGTAAGTAAAGCGTTGG 408
DB 133 GTCAACGTATTCAGGGCGATGCACACAGCAACGAGGCTGATTAAGATTAAGGCAAG 252

QY 409 TCGAATTCGAATTGCTATGATATCTTAATTAACCTAGTCAAACTTCGATGGGATTTGAT 468
DB 253 GAAATCTCTACATTTCTCCGGCTTCCAGACCCGGGATTAAGACGCTCTG-----ACT 306

QY 469 GGTAAAGCTTGAATGCTTGTGATGCGTTGAAACCTAAGACCGGAGGTTACCGGAT 528
DB 307 CCGGAGGCGTGACAAAGGTTCTCGAAGACTGAA-----GAAATGAATTCGAT 357

QY 529 TTCATCATCATGATTTGCTCTGAGAAATCGATGCGGATTCATAACCGCATTACTCCG 588
DB 358 TTCATCGTGTGATTTCCCGGAGGATTTGAACCGGTCGCTGATGGCGCTTAATTT 417

QY 589 GCGAATGAAGAGTTCTGTGTAACAACCTCCGATATTAACGCGTTAAGGATGCTGA 644
DB 418 GCTGATGAAGCATCATCACCACTAACCCGGAAGTCTCTCGTTGCGACTCCGA 473

RESULT 5
US-09-252-991A-5063
; Sequence 5063, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 5063
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; LENGTH: 822
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-5063

Query Match
Best Local Similarity 8.2%; Score 79.8; DB 4; Length 822;
Matches 135; Conservative 0; Mismatches 92; Indels 0; Gaps 0;

QY 178 ATCGTGTATCACTCCGGAAGAGCGGTGTGAAGAAGCAACCAACCGCAATGTC 237
DB 16 ATCTGTAAGTACTTCGGTAAGGTGCGTGGTAAACCAACCAACCGCAAGTATC 75

QY 238 GGTCTCTCTCGCTCGTTACCGTTTCTCAGTTTTCGCCATTGACCGGACCTTGCTC 297
DB 76 GGCACGCGCGCTGCGCTTGGCGGTTTCAAGACCGTCACTGCTGACTTGGAGCTGCGGCTG 135

QY 298 CGTAACCTCGATCTCCTCTAGGGTTAGAGAAATCGATCAATTACCTTGCCTGAGGTT 357
DB 136 CGTAACCTCGAACCCTATCATGAGGCTGCGAAGCCCGCTGTGTACGACTTGTCAACGTC 195

QY 358 ATTAACGAGATTGTCGTCTCGATCAAGCTCTGTACGATGATAGCG 404
DB 196 GTCAACGGGAGGAGCCCTCAACCAAGGCTGTATCAAGACAAAGCG 242

RESULT 6
US-09-252-991A-5154/C
; Sequence 5154, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 5154
; LENGTH: 903
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-5154

Query Match
Best Local Similarity 8.2%; Score 79.8; DB 4; Length 903;
Matches 135; Conservative 0; Mismatches 92; Indels 0; Gaps 0;

QY 178 ATCGTGTATCACTCCGGAAGAGCGGTGTGAAGAAGCAACCAACCGCAATGTC 237
DB 876 ATCTGTAAGTACTTCGGTAAGGTGCGTGGTAAACCAACCAACCGCAAGTATC 817

QY 238 GGTCTCTCTCGCTCGTTACCGTTTCTCAGTTTTCGCCATTGACCGGACCTTGCTC 297
DB 816 GGCACGCGCGCTGCGCTTGGCGGTTTCAAGACCGTCACTGCTGACTTGGAGCTGCGGCTG 757

QY 298 CGTAACCTCGATCTCCTCTAGGGTTAGAGAAATCGATCAATTACCTTGCCTGAGGTT 357
DB 756 CGTAACCTCGAACCCTATCATGAGGCTGCGAAGCCCGGTGTGTAGCACTTGTCAACGTC 697

QY 358 ATTAACGAGATTGTCGTCTCGATCAAGCTCTGTGTAAGTAAAGCG 404
DB 696 GTCAACGGGAGGAGCAACCTCAACCAAGGCTGTATCAAGACAAAGCG 650

RESULT 7
US-09-596-002-13/C
; Sequence 13, Application US/09596002
; Patent No. 6632636
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; GENERAL INFORMATION:
; APPLICANT: Lagace, Robert, E.
; APPLICANT: Paterson, Chandra
; APPLICANT: Berg, Kim, L.
; TITLE OF INVENTION: NUCLEOTIDE SEQUENCES OF MORAXELLA CATARRHALIS GENOME
; FILE REFERENCE: PM-0008-4 US
; CURRENT APPLICATION NUMBER: US/09/596,002
; PRIOR FILING DATE: 2000-06-16
; PRIOR APPLICATION NUMBER: 60/140,121
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PERL Program
; SEQ ID NO 13
; LENGTH: 31940
; TYPE: DNA
; ORGANISM: M. catarrhalis
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte template ID No. 6632636 13
; PUBLICATION INFORMATION:
; US-09-556-002-13

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Query Match
Best Local Similarity 54.2%; Score 73; DB 4; Length 31940;
Matches 148; Conservative 0; Mismatches 125; Indels 0; Gaps 0;

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QY 178 ATGTGCTATACCTCCGGAAGAGCGGTGTGGAAGACGACCAACCGCAATGTC 237
DB 273 ATGTGCTATACCTCCGGAAGAGCGGTGTGGAAGACGACCAACCGCAATGTC 237
QY 238 GGCTCTCTCTCGCTGCTTACGCTTTCATGTTGCGCATGACCGCATTTGCTGC 297
DB 213 GGTGAGAGGCTTCTGCTTACGCTTTCATGTTGCGCATGACCGCATTTGCTGC 297
QY 298 CGTACCTGATCTCTCTCTGAGGTTAGAGATCGATGCAATTAACCTTGCAGGTT 357
DB 153 CGTACCTGATCTCTCTCTGAGGTTAGAGATCGATGCAATTAACCTTGCAGGTT 357
QY 358 ATAAACGAGATTGCTGCTGATCAAGCTTGGTACGTATAGCGTTGCTGCAATTC 417
DB 93 ATCAGTGTATGCGACAGCTTCTCAAGCCTTAGTCAAAACAAATTTGAAATCTA 34
QY 418 GAATTCGTATGTATTTAAACCTAGATCGAAA 450
DB 33 TACATTTTGCTGCTGATCGAAACGCGACAAA 1

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RESULT 8
US-09-790-988-1/c
; Sequence 1, Application US/09790988
; Patent No. 6632935
; GENERAL INFORMATION:
; APPLICANT: SHIGENOBU, SHUJI
; APPLICANT: WATANABE, HIDEKI
; APPLICANT: HATTORI, MASAHIRA
; APPLICANT: SAKAKI, YOSHIYUKI
; TITLE OF INVENTION: GENOME DNA OF BACTERIAL SYMBIONT OF APHIDS
; FILE REFERENCE: 081356/015
; CURRENT APPLICATION NUMBER: US/09/790,988
; PRIOR FILING DATE: 2001-02-23
; PRIOR APPLICATION NUMBER: JP2000-107160
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 640681
; TYPE: DNA
; ORGANISM: Buchnera sp.
; US-09-790-988-1

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Query Match
Best Local Similarity 47.1%; Score 65; DB 4; Length 640681;
Matches 249; Conservative 0; Mismatches 265; Indels 15; Gaps 1;

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QY 167 AAAGCCGCTATGCTGTTATGACCTCCGGAAGAGCGGTGTGGAAGACGACCA 226
DB 36254 ATATGACACGGAATTAATTTAGTACTTACGAGGAAGAGGTTAGTAACTTCAA 362465
QY 227 CCGGAATGTCGGTCTCTCTGCGTCGCTTACGCTTTCTGAGTTGCGCAATTCGCG 286
DB 362464 GTGACGCTATCCGGAAGAGTTTACGACAAAAGGAAAAAACAATGTTATAGCTTTG 362405
QY 287 ACCGTGCTCCGTTAACTCGATCTCTCTAGGTTAGAAATCGATCAATTAACCTT 346
DB 362404 ATATGAGATTGAGAAATTTAGATTAATTAAGGATGGAACGTAGTACTTATGACT 362345
QY 347 GCGTCAGGTTATTAACGAGATGCTGCTCGATCAAGCTTGTATAGATTAAGCTT 406
DB 362344 TTATTAATGTTATTAAGATGATGACACCTTAATCAAGCAATTAATTAAGATTA 362285
QY 407 GGTCAATTTGCAATGCTATGATATCTTAACCTTAGATGAAACTCCGATGGATTG 466
DB 362284 CAATTAATTTGTTATTAATCACTCATCAAACTGATTA-----G 362240
QY 467 GTGTAAAGCATTTGAATGCTTGTGATGCTTGAATACTAGACGGAAGTTCAACCG 526
DB 362239 ACGCTTTAACAGATAGAGATTGAATAAGTTTAAACAGAACTTATTAATAATTTG 362180
QY 527 ATTTTCATCATGATGATTTGCTGCAAGATCGATCCGGAATTCATTAACCGCATTAAC 586
DB 362179 ATTTATATTTTGTGATTCACAGAGGATTAACGGGTGCTATTTAGCAATATAT 362120
QY 587 CGGGAATGAAGAGATTTCTGTAAACAATCCGATATTAACAGCTTAAAGATGCTGATA 646
DB 362119 TTGAGATGAAGATATTTATTAATTAACCCGAAAGTTCTTCACTAGAGATTCGATC 362060
QY 647 GGGTTACGGTTTGTATGATGCGATGAATCAGAGATTAATAAGATGAT 695
DB 362059 GAATTTAGAAATTAATTCATTAATCAAAAAGAGCTGAGAAAAACAT 362011

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RESULT 9
US-08-916-421B-1
; Sequence 1, Application US/08916421B
; Patent No. 6503729
; GENERAL INFORMATION:
; APPLICANT: Built et al.
; TITLE OF INVENTION: Complete Genome Sequence of the Methanogenic Archaeon, Methanococcus
; FILE REFERENCE: jamaeschi1
; CURRENT APPLICATION NUMBER: US/08/916,421B
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: US 60/024,428
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 1664976
; TYPE: DNA
; ORGANISM: Methanococcus jamaeschi1
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (28222)..(28222)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (28257)..(28258)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (84773)..(84773)
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; NAME/KEY: misc feature
; LOCATION: (84808)..(84808)
; OTHER INFORMATION: n equals a, t, c, or g
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; LOCATION: (84812)..(84812)

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LOCATION: (1119881) .. (1119881)
OTHER INFORMATION: n equals a, t, c, or g
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OTHER INFORMATION: n equals a, t, c, or g
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LOCATION: (1313224) .. (1313224)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc_feature
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OTHER INFORMATION: n equals a, t, c, or g
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OTHER INFORMATION: n equals a, t, c, or g

US-08-916-421B-1
Query Match 5.2%; Score 50.6; DB 4; Length 1664976;
Best Local Similarity 59.3%; Pred. No. 0.00039;

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Matches 86; Conservative 0; Mismatches 59; Indels 0; Gaps 0;
OY 182 TCGTATACCTCCGAAAGCGCGTGTGAAAGACGACACCGCAAAATGTCGTC 241
DB 987966 TCGGATAGCATCTGGAAGAGGTACTGMAAGCAAGATATCTGCAAACTTGTGCG 988025
OY 242 TCTCTCGCTCGTGTAGCGTTTCTCAAGTTGTCGCCATTGACGCCGACCTTGTCTCCGTA 301
DB 988026 TGGCTTTGGCAAAATTGGAAAAAGTGGCTGTTTGGACGCTGATATAGCAATGGCA 988085
OY 302 ACCCGCATCTCTCTCTAGGGTTAGA 326
DB 988086 ACTTAGAGCTTATCATAGGGTTAGA 988110

RESULT 10
US-09-692-570-1
/ Sequence 1, Application US/09692570
/ Patent No. 6797466
/ GENERAL INFORMATION:
/ APPLICANT: Bult et al.
/ TITLE OF INVENTION: Complete Genome Sequence of the Methanogenic Archaeon, Methanoco-
/ Patent No. 6797466
/ TITLE OF INVENTION: jannaschii
/ FILE REFERENCE: PB275C1
/ CURRENT APPLICATION NUMBER: US/09/692,570
/ PRIOR FILING DATE: 2003-01-14
/ PRIOR APPLICATION NUMBER: US 60/024,428
/ PRIOR FILING DATE: 1996-08-22
/ PRIOR APPLICATION NUMBER: US 08/916,421
/ NUMBER OF SEQ ID NOS: 20
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 1
/ LENGTH: 1664976
/ TYPE: DNA
/ ORGANISM: Methanococcus jannaschii
/ FEATURE:
/ NAME/KEY: misc_feature
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/ OTHER INFORMATION: n equals a, t, c, or g
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/ OTHER INFORMATION: n equals a, t, c, or g
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; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 3142
; SEQ ID NO 1056
; LENGTH: 1134
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-1056

Query Match      4.4%; Score 42.6; DB 4; Length 1134;
Best Local Similarity 61.1%; Pred. No. 0.0018;
Matches 69; Conservative 0; Mismatches 44; Indels 0; Gaps 0;

Oy 178 ATGTGTTATCACTCCGAAAAAGCGGCTGTGAAAGCAGCAACACCGCAATGTC 237
Db 340 ATGTGTCGGTGCGCTTCGCGCAAGGCGGGCGGTGCGAATCCACCAACCGCAACTG 399
Oy 238 GGTCCTCTCTGCGTCGTGAAGGTTTCTAGTGTGTCGCAATGACGCCGACT 290
Db 400 GCCCTGGCCTTGCCCGCGAAGGCTGCCGCGTGGGATCTCTGACGCGAAT 452

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RESULT 14
 US-09-252-991A-904/C
 ; Sequence 904, Application US/09252991A
 ; Patent No. 6551795
 ; GENERAL INFORMATION:
 ; APPLICANT: Marc J. Rubenfield et al.
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
 ; FILE REFERENCE: 107196.136
 ; CURRENT APPLICATION NUMBER: US/09/252,991A
 ; CURRENT FILING DATE: 1999-02-18
 ; PRIOR APPLICATION NUMBER: US 60/074,788
 ; PRIOR FILING DATE: 1998-02-18
 ; PRIOR APPLICATION NUMBER: US 60/094,190
 ; PRIOR FILING DATE: 1998-07-27
 ; NUMBER OF SEQ ID NOS: 3142
 ; SEQ ID NO 904
 ; LENGTH: 1254
 ; TYPER: DNA
 ; ORGANISM: *Pseudomonas aeruginosa*
 US-09-252-991A-904

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Query Match          4.4%; Score 42.6; DB 4; Length 1254;
Best Local Similarity 61.1%; Pred. No. 0.0019;
Matches 69; Conservative 0; Mismatches 44; Indels 0; Gaps 0

Qy      178  ATCGTCGTTTCACCTCCGGAAGAAAGCGGTGTTGGAAAAGACACACACCGCAAAATGTC 237
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Db      933  ATGTCGCGGTGGCTTCGCGCAAGGCGCGTCGCGCAAGTCACACACCGCGCCAACTG 874

Qy      238  GGTCTCTCTCCGTCGTTACGGTTTCTCAATTGTCCGCAATGACGCCGACT 290
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Db      873  GCCCTGGCCTTGGCCCGCGAAGGTGCGGCGTGGCAATCTTCGACGCGGCACT 821

RESULT 15
US-09-221-017B-1015/C
; Sequence 1015, Application US/09221017B
; Patent No. 6444799
; GENERAL INFORMATION:
; APPLICANT: ROSS, BRUCE C.
; TITLE OF INVENTION: P. GINGIVALIS NUCLEOTIDES AND USES THEREOF
; NUMBER OF SEQUENCES: 1120
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 PAGE MILL ROAD
; CITY: PALO ALTO
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1018
COMPUTER READABLE FORM.

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: March 10, 2005, 20:49:08 / Search time 606 Seconds
(without alignments)
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Title: US-09-553-431B-1

Perfect score: 978

Sequence: 1 atgcgcctctcgaatttgtt.....tctctcttcttcttgscgcgc 978

Scoring table: IDENTITY_NUC

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- 12: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
- 13: /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
- 14: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
- 15: /cgn2_6/ptodata/2/pubpna/US10C_PUBCOMB.seq:*
- 16: /cgn2_6/ptodata/2/pubpna/US10D_PUBCOMB.seq:*
- 17: /cgn2_6/ptodata/2/pubpna/US10F_PUBCOMB.seq:*
- 18: /cgn2_6/ptodata/2/pubpna/US10F_PUBCOMB.seq:*
- 19: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
- 20: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq:*
- 21: /cgn2_6/ptodata/2/pubpna/US66_NEW_PUB.seq:*
- 22: /cgn2_6/ptodata/2/pubpna/US66_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	480.2	49.1	1419	US-10-424-599-74906	Sequence 74906, A
2	341.6	2866	18	US-10-739-930-1807	Sequence 1807, Ap
3	325.6	33.3	1183	US-10-767-701-7575	Sequence 7575, Ap
4	320	921	18	US-10-437-963-49916	Sequence 49916, A
5	237.4	24.3	2435	US-10-425-115-119462	Sequence 119462, A
6	154.2	15.8	521	US-10-021-323-6876	Sequence 6876, Ap
7	153	15.6	495269	US-10-398-221-8	Sequence 8, Appl
8	145.4	14.9	406	US-10-396-221-2058	Sequence 2058, Ap
9	143.8	14.7	545	US-10-424-599-76259	Sequence 76259, A
10	143.8	14.7	545	US-10-021-323-8529	Sequence 8529, Ap
11	132.4	13.5	547	US-10-767-701-26469	Sequence 26469, A

C 12	105	10.7	1987	17	US-10-398-221-3303	Sequence 3303, Ap
C 13	87.6	9.0	2731748	18	US-10-297-465A-1	Sequence 1, Appl1
C 14	81.4	8.3	807	17	US-10-335-977-3900	Sequence 3900, Ap
C 15	73	7.5	31940	17	US-10-672-787-13	Sequence 13, Appl
C 16	69.2	7.1	891	17	US-10-425-114-33547	Sequence 33547, A
C 17	68.6	7.0	499	18	US-10-425-115-15105	Sequence 15105, A
C 18	67.6	6.9	996	18	US-10-425-115-15107	Sequence 15107, A
C 19	65	6.6	640681	9	US-09-790-988-1	Sequence 1, Appl1
C 20	54.6	5.6	379	18	US-10-425-115-101244	Sequence 101244, A
C 21	46.4	4.7	2256646	18	US-10-470-565-1	Sequence 1, Appl1
C 22	42.8	4.4	885	17	US-10-335-977-4514	Sequence 4514, Ap
C 23	42.8	4.4	891	17	US-10-335-977-4515	Sequence 4515, Ap
C 24	42.4	4.3	513	17	US-10-335-977-4513	Sequence 4513, Ap
C 25	42.2	4.3	1107	17	US-10-335-977-3163	Sequence 3163, Ap
C 26	42.2	4.3	1236	17	US-10-335-977-3164	Sequence 3164, Ap
C 27	42.2	4.3	1239	17	US-10-335-977-3165	Sequence 3165, Ap
C 28	42.2	4.3	1275	17	US-10-335-977-3166	Sequence 3166, Ap
C 29	42	4.3	401	9	US-09-974-300-4671	Sequence 4671, Ap
C 30	42	4.3	2793	13	US-10-194-163-1015	Sequence 1015, Ap
C 31	40	4.1	282	17	US-10-335-977-3899	Sequence 3899, Ap
C 32	40	4.1	285	17	US-10-335-977-3898	Sequence 3898, Ap
C 33	39.8	4.1	1047	17	US-10-282-122A-25652	Sequence 25652, A
C 34	38.6	3.9	303	18	US-10-425-115-121114	Sequence 121114, A
C 35	38.2	3.9	837	9	US-09-738-626-3425	Sequence 3425, Ap
C 36	37.4	3.8	30601	10	US-09-373-658-33	Sequence 33, Appl
C 37	37.4	3.8	30601	11	US-09-989-687-33	Sequence 33, Appl
C 38	37.4	3.8	30601	11	US-09-989-687-33	Sequence 33, Appl
C 39	37	3.8	629	18	US-10-767-701-15140	Sequence 15140, A
C 40	37	3.8	768	18	US-10-767-701-15233	Sequence 15233, A
C 41	37	3.8	1038	15	US-10-156-761-6485	Sequence 6485, Ap
C 42	37	3.8	1392	18	US-10-767-701-15405	Sequence 15405, A
C 43	37	3.8	1449	17	US-10-369-493-31810	Sequence 31810, A
C 44	37	3.8	6307	17	US-10-221-714A-504	Sequence 504, App
C 45	37	3.8	6521	15	US-10-311-455-1929	Sequence 1929, Ap

ALIGNMENTS

RESULT 1
US-10-424-599-74906
Sequence 74906, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53223)B
CURRENT APPLICATION NUMBER: US/10/424,599
NUMBER OF SEQ ID NOS: 285684
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 74906
LENGTH: 1419
TYPE: DNA
ORGANISM: Glycine max
FEATURE:
OTHER INFORMATION: Clone ID: PAT_MRT3847_38653C.1
US-10-424-599-74906
Query Match 49.1%, Score 480.2, DB 17, Length 1419,
Best Local Similarity 70.2%, Pred. No. 1e-142,
Matches 644, Conservative 0, Mismatches 273, Indels 0, Gaps 0,
QY 58 CTCCTCAAAAGACTATATCTTACCAAGATTCGCAATTAACCTAGACGAGT 117
DB 81 CCGCCCATTCCTCCCTCTCTCCCTCCCAAAACCTTAACCCCAAAACCCAAACCCAA 140
QY 118 CCAATAGATCGTCTTCAATTATTAATGCAAAACGAACTCGCCGAGAAACGCGGT 177
DB 141 CCCCCAGTGCCTGCGCCCAATGAACCCGACGCGAGCTCCGCGTCCATCCGCGC 200

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QY 178 ATCCGCTTATCACTCCGGAAGGCGGTGTTGAAAGAGCAACCAACCGGAATGTC 237
Db 201 GTACCGTATTAATCCCGGAAAGGGCGGTGGCAAGACACACACCGCAATC 260
QY 238 GGTCTCTCTCGCTCGCTTAAGTTTCTCAGTTGTGGCCATTACCGCGCACTTGGTCTC 297
Db 261 GGCCTCTCTCGCTCGCTTAAGTTTCTCAGTTGTGGCCATTACCGCGCACTTGGTCTC 320
QY 298 CGTAACCTCGATCTCTCTCGCTTAAGTTTCTCAGTTGTGGCCATTACCGCGCACTTGGTCTC 357
Db 321 CGCAACTCGATCTCTCTCGCTTAAGTTTCTCAGTTGTGGCCATTACCGCGCACTTGGTCTC 380
QY 358 ATAAACGGAATTTGCTCTCGCTTAAGTTTCTCAGTTGTGGCCATTACCGCGCACTTGGTCTC 417
Db 381 CTCAACGGGAGTCCCGCTCGCAAGCCCTGCTCGCAAGGGCTGTCCTCACTTGGTCTC 440
QY 418 GAATTCGATATATCTTAACCTAGATGAACCTTCCGATGGAGTTTGGTGTAAAGCA 477
Db 441 GAATTCCTCTGATCTTCAACCCCGCTCAAGCTTCCCTTGGCTTGGCGGTAAAGCC 500
QY 478 TTGGAATGGCTTGGATGCTTGAAGAACTAGACCGGAAGTTTACCGGATTTGATGATC 537
Db 501 CTCACTGGCTGTGGAGCGCTGTAAGGCGGTTCACAGGGCTCCCTGATCTTATCTC 560
QY 538 ATCGATTTGCTGCAAGGATCGATCCGGAATTCATTAACCGCAATTACTCCGCGCAATGA 597
Db 561 ATCGATTTGCTGCAAGGATCGATCCGGAATTCATTAACCGCAATTACTCCGCGCAATGA 620
QY 598 GCAATTCGTTAACTCCGGAATTAACCGGATTAAGGATGCTGATAGGATTAACGGT 657
Db 621 GCGGCTCTATCAACCCCGCAATCAACGCTCCGCAAGCGCGCAAGCGCTCACCGG 680
QY 658 TTGTTAGAATCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 717
Db 681 CTCTCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 740
QY 718 ATGATTAAGGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 777
Db 741 ATGATTAAGGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 800
QY 778 TTGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 837
Db 801 TTGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 860
QY 838 CTGTTCTGAATAAGCTCTTACGCTTGGGGAATTTGGCTTTGAGCAGCGCTTGGAGA 897
Db 861 CTGTTCTGAATAAGCTCTTACGCTTGGGGAATTTGGCTTTGAGCAGCGCTTGGAGA 920
QY 898 CTGTTGAGCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 957
Db 921 CTGTTGAGCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 980
QY 958 TTCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 974
Db 981 TTCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 997

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RESULT 2

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US-10-739-930-1807
; Sequence 1807, Application US/10739930
; Publication No. US20040216190A1
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES AND OTHER MOLECULES ASSOCIATED WITH
; FILE REFERENCE: 38-21(53377)B
; CURRENT APPLICATION NUMBER: US/10/739,930
; NUMBER OF SEQ ID NOS: 2003-12-18
; SEQ ID NO 1807
; LENGTH: 2886
; TYPE: DNA

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; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: ZEANA-23APR03-CLUSTER13300_1
US-10-739-930-1807

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Query Match 34.9%; Score 341.6; DB 18; Length 2886;
Best Local Similarity 65.5%; Pred. No. 4.8e-98;
Matches 516; Conservative 0; Mismatches 269; Indels 3; Gaps 1;

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QY 151 CCGGAATCGGCGGAGAAAGCCGCTATGCTGTTATCACTCCGGAAGGCGGTGTT 210
Db 291 CCGGAGCTCTCGGAGCCGAGCCCGCGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 350
QY 211 GGAAGACGACACCAACCGCAATGTCGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 270
Db 351 GGAAGACGACACCAACCGCAATGTCGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 410
QY 271 GTGCGCATTAAGCGGAGCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 330
Db 411 GTGCGCATTAAGCGGAGCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 470
QY 331 CGAGTCAATTAACCTTGGCTGAGGTTAATGAAGGATGTTGTGTGTGTGTGTGTGTGTGTGT 390
Db 471 CGCGTCCACTCACCGCGCGCGAGTCTCTCGGAGATGTCGACTTCGACCGAGCGCTC 530
QY 391 GTAGTGAATTAAGCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 450
Db 531 GTGCGCATTAAGCGGAGCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 590
QY 451 CTTCGATGAGATTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 510
Db 591 CTGCGCTCGGTTGCGATTCAGAACCTTCACTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 570
QY 511 CCGGAAGTTTACCGGATTTGATCATCATCATCATCATCATCATCATCATCATCATCATCATCAT 630
Db 648 TCGACACCGCCACCGCATTTATCTCATCATCATCATCATCATCATCATCATCATCATCATCAT 707
QY 571 ATAAACCGCATTAATCTCCGCAATGAGGATGTCGTTGTTAAAGGAGATGATGATGATGAT 630
Db 708 GTCACTGCTATTCACCGCGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 767
QY 631 TTAAGGAGTCTGATGAGGTTACGGCTTTGTTAGATGATGATGATGATGATGATGATGATG 690
Db 768 CTCCGCGATGCTGACCGGTCTCGGAGCTGCTGAGTGCATGAGGATCAAGACATCAAG 827
QY 691 ATGATTTGAACAGATGAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 750
Db 828 ATGATTTGAACAGATGAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 887
QY 751 GATGTCAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 810
Db 888 GATGTCAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 947
QY 811 ATTGAAGCAGAAATCAGAGGTTCCGCTTGTCTGAATAAGCTCTTACGCTTGGGGA 870
Db 948 ATCCGAGTACGATTAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1007
QY 871 TTGCGTTGAGCAGGAGGCTTGAAGCTGTTGAGCAGATGATGATGATGATGATGATGATGAT 930
Db 1008 CTGCTCTGAGGAGGCTTGAAGCTGTTGAGCAGATGATGATGATGATGATGATGATGATG 1067
QY 931 GTGAGAGA 938
Db 1068 GTCGAGAGA 1075

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RESULT 3

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US-10-757-701-7575
; Sequence 7575, Application US/10767701
; Publication No. US20040172684A1
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua

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APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE OF INVENTION: Plants and Uses Thereof For Plant Improvement
; FILE REFERENCE: 38-21(5355)B
; CURRENT APPLICATION NUMBER: US/10/767,701
; CURRENT FILING DATE: 2004-01-29
; NUMBER OF SEQ ID NOS: 63128
; SEQ ID NO 7575
; LENGTH: 1183
; TYPE: DNA
; ORGANISM: Sorghum bicolor
; FEATURE:
; OTHER INFORMATION: Clone ID: SORBI-28MAY03-CLUS93226_1
US-10-767-701-7575

Query Match      33.3%; Score 325.6; DB 18; Length 1183;
Best Local Similarity 64.2%; Pred. No. 3.9e-93;
Matches 506; Conservative 0; Mismatches 279; Indels 3; Gaps 1;

QY 151 CCGGAACCTCGCGGAGAAACCGCGGATCCGCTTATACCTCCGGAAAGCGGATGT 210
DB 121 CCGGAGCTCTCGGCGCCGACCCCGCGCGTGTGTGTCTACCTCCGGAAAGCGGCGTC 180
QY 211 GGAAGACGACAAACCAACCGCAATGTCGCTCTCTCTGCTGTTACGGTTTCTCAGTT 270
DB 181 GCGAAGACCAACCACTACCGCCCACTCGCGCGCTGCTGCGCGCTCGGACTCCCCGCC 240
QY 271 GTGCGCATTTAGACCGGACCTTGTCTCGGTAACCTCGATCTCTCTCTTAAAGGTTAGAGANT 330
DB 241 GTGCGCGTGTGACCGCGACCGCGCGCTCCGCAACCTCGACCTCTGCTCGGCTCGAAGAAC 300
QY 331 CGAGTCATTTACATTTGCTGTGAGTTTAAACGAGATTGTCTGTCTGATCAAGTCTG 390
DB 301 CGCGTCACCTTACACCGCGCGCGACGCTCGCTGGGAGCTGAGGCTGCACAGGCGCTC 360
QY 391 GTACGTGATTAAGCGTTGTGTGATTTGCAATTGCTATGATTAACCTAGATCGAANA 450
DB 361 GTCCGACACCGCGCGCTCCAGAGACTTCCACTCTCTCTCTCTCCAGCGACGCTCGAAG 420
QY 451 CTTCCGATGGAATTTGTGTGTAAGCAATTTGATGAGTGGCTTTGTGATGCGTTGAAACTAGA 510
DB 421 CTGCGCGTGGGCTTGGGATTCGAAGACCTTCACTGGGTGCGCGAGCGCT--TCGGCGC 477
QY 511 CCGGAAGGTTACCGGATTTTATCATATCATGATTTGCTCTGCGAAGATTCATGCGCGATTC 570
DB 478 TCGCGTAAACACCGCGCTTCAATCTCATGACTGCTGCGCGAGGTGTTGATCCGGGTTT 537
QY 571 ATTAACCGCATTAATCTCGCGGATTAAGGAGATTCTGTAACAACCTCGGATTTAAACAGCG 630
DB 538 GTCACTGCCATTTGCACTGCGAGAGAGGAGAGTGTCTGTTACCAACCTTGAACATTAGCGCT 597
QY 631 TTAAGGATGCTGATAGGGTTACGGGTTTGTAGATGCGATGGAATCAGAGATATTAAG 690
DB 598 CTCGCGATGCTGACGCTGTCCGAGAGCTGTGAGATGCGATGCGATCAAGATATCAAG 657
QY 691 ATGATTTGTAACAGAGTGAAGTGTATGATTTAAAGGAGAGATATGATGTCAGTTGA 750
DB 658 ATTATTTGTAACCGGATGCGGACGCTGATGAAGGAGGAGAGATGATGTCAGGCTT 717
QY 751 GATGTCAGAGAGATGTTGGGATTTGATGCTGTTGATTAATTCGTAAGATTCTGAGTT 810
DB 718 GATGTCGAAGAAATGTTGGCTTGTGCTTGTGTTGTTGCTTCTGAGAGCGCGAGGTT 777
QY 811 ATTGAAGACGAATGAGGGTTTCCGCTTGTCTGTAATTAAGCTTCTTACGCTTGGCGGA 870
DB 778 ATCCGAGATTAATAATGAGGGTGTGCAATTTGTGCTCAACGACCGCGCAACGCTGGGCG 837
QY 871 TTGGCGTTGAGACGCGGCTTGAAGCTGCTTTGAGCAAGATATGATGAAGCTGTTAAG 930
DB 838 CTTGCTCTGAGACGAGCTGCTGCGATTTGTGGAAGAGATGCGATGACAGAGTCATG 897
QY 931 GTGAGGA 938
| | | | |
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DB 898 GTGAGGA 905

RESULT 4
US-10-437-963-49916
; Sequence 49916, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 49916
; LENGTH: 921
; TYPE: DNA
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_52454C.1
US-10-437-963-49916

Query Match      32.7%; Score 320; DB 18; Length 921;
Best Local Similarity 63.3%; Pred. No. 2.1e-91;
Matches 529; Conservative 0; Mismatches 295; Indels 12; Gaps 2;

QY 151 CCGGAACCTCGCGGAGAAACCGCGGATCGTGTATACCTCCGGAAAGCGGATGT 210
DB 85 CCGGAGCTCTCGGCGCCGACCCCGCGCGTGTGTGTCTACCTCCGGAAAGCGGCGTG 144
QY 211 GGAAGACGACAAACCAACCGCAATGTCGCTCTCTCTGCTGTTACGGTTTCTCAGTT 270
DB 145 GGTAAAGACCAACCAACCGCGCAATGTCGCGCGCTCCCTGCAAGGCTCTCCCTCGCGC 204
QY 271 GTGCGCATTTAGACCGGACCTTGTCTCGGTAACCTCGATCTCTCTCTTAAAGGTTAGAGANT 330
DB 206 GTGCGCGTGTGACCGCGACCGCGCGCTGCGCAATCTGAGACTCTCTCGGCTCGAAGAC 264
QY 331 CGAGTCATTTACATTTGCTGTGAGTTTAAACGAGATTGTCTGTCTGATCAAGTCTG 390
DB 265 CGCGTCACCTTACACCGCGCGCGACGCTGCTGGGAGACTGCGCGCTCGACAGGCGCTC 324
QY 391 GTACGTGATTAAGCGTTGTGTGATTTGCAATTGCTATGATTAACCTAGATCGAANA 450
DB 325 GTCCGACACCGCGCGCTCCATGACCTGCACTGCTCTGCTCTCCAGCGCGCTCAAG 384
QY 451 CTTCCGATGGAATTTGTGTGTAAGCAATTTGATGAGTGGCTTTGTGATGCGTTGAAACTAGA 510
DB 385 CTGCGCGTGGGCTTGGGATTCGAAGACCTTCACTGGGTGCTGAGCGCT--TCGCGC 441
QY 511 CCGGAAGGTTACCGGATTTTATCATATCATGATTTGCTCTGCGAAGATTCAGATGCGGATTC 570
DB 442 GCGCGCAACCAACCGCGCTTTCATCTCATGACTGCTGCGAGAGTGTATGAGAGGTTT 501
QY 571 ATTAACCGCATTAATCTCGCGGATTAAGGAGATTCTGTAACAACCTCGGATTTAAACAGCG 630
DB 502 GTCACTGCTATTGCTTCCGCAAGAGGCGGCTTGTATCAACCTTGAACATTAGCGCT 561
QY 631 TTAAGGATGCTGATAGGGTTACGGGTTTGTAGATGCGATGGAATCAGAGATATTAAG 690
DB 562 CTCGCGATGCTGACGCTGTGCAAGGCTTATGAGTGTGAGGCTTCAAGATTAAG 621
QY 691 ATGATTTGTAACAGAGTGAAGTGTATGATTTAAAGGAGAGATATGATGTCAGTTGA 750
DB 622 ATTATTTGTAACCGGATGCGGACGCTGATGAAGGAGAGATATGATGTCAGGCTT 681
| | | | |
```

QY 751 GATGTGACGAGATGTTGGATTTGTCTATTCCTGTGATTTCTGAAATTCGATG 810
 Db 682 GATTTTAAAGAAAGCTTGGCTTCTTCTAGTGTGTGTGCAAGAGACGGAGGTG 741
 QY 811 ATTCGAAGACGAATCGAGGGTTTCGCTTGTCTGAATTAAGCTTCTTAAGCTTGGAG 870
 Db 742 ATCCGAGTACAAATATAGAGTGTGCGGTGTCTGAAGACCCACACCACTGCTGT 801
 QY 871 TTGGCGTTTGAAGCGCGCTTGGAGACTGTGACAAATATATGAAAGGCTGTATG 930
 Db 802 CTTCCTCTGAGAGCGGACTTGGCGGTGTGTGAAGAGATGCAATGACAGCACTTATG 861
 QY 931 GTGAGGAGAG-----ACCTAGAAACGTGCTTCTTCTTTTGGCGG 977
 Db 862 GTAGAGGACGAGAGAGGCGCCAAAGAAAGCTGGGTTCTTCTTCTTGTGTG 917

RESULT 5
 US-10-425-115-119462/c
 / Sequence 119462, Application US/10425115
 / Publication No. US20040214272A1
 / GENERAL INFORMATION:
 / APPLICANT: La Rosa, Thomas J.
 / APPLICANT: Kovalic, David K.
 / APPLICANT: Zhou, Yihua
 / APPLICANT: Cao, Yongwei
 / TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
 / FILE REFERENCE: 38-21(53222)B
 / CURRENT APPLICATION NUMBER: US/10/425,115
 / CURRENT FILING DATE: 2003-04-28
 / NUMBER OF SEQ ID NOS: 369326
 / SEQ ID NO 119462
 / LENGTH: 2435
 / TYPE: DNA
 / ORGANISM: Zea mays
 / FEATURE:
 / OTHER INFORMATION: Clone ID: MFT4577_40432C.1
 US-10-425-115-119462

Query Match 24.3%; Score 237.4; DB 18; Length 2435;
 Best Local Similarity 63.8%; Pred. No. 1.2e-64;
 Matches 377; Conservative 0; Mismatches 211; Indels 3; Gaps 1;
 QY 348 CGTCGAGGTTATTAACGAGATTTGTCTCTGATCAAGCTTGTGATTAAGCTTGG 407
 Db 2399 CGCCGAGCTCTCGCGGAGACTGCGGACTCGACCTGACCAAGGCGCTGTCCGCCACCGCGCT 2340
 QY 408 GTGGAATTTGGAATTCGTATGTAATCTTAACCTAGATCGAAACTTGGATGGATTTGG 467
 Db 2339 CCACGACCTCCACCTCTCTGCTCTCCAAAGCCCGCTCCAAAGCTGCGCTGTGCG 2280
 QY 468 TGTGAAGCATTTGAATGGCTTGTGAGTGGCTTGAACCTAGACCGGAAGTTGACCGGA 527
 Db 2279 ATCCAAAGACCTCACCCTGAGGTGCGGAGCGCTACGAC---GCTCGACACGACCCACCGC 2223
 QY 528 TTTTCATCATCATCATGATTTGTCTCTGCAAGATGATGCGGATTTCAATACCGCATTAATCC 587
 Db 2222 ATTCAATCCATCATGACTGCGCGGAGGTGTGATGCTGGTTTCTCCTGCAATGGACC 2163
 QY 588 GCGGATGAGAGAGTTCTGTGTAACAATCCGAGATTAACAGCGTTAAGGATGCTGATAG 647
 Db 2162 CGCAAAAGAGCGGCTGCTGTGTAACATCCCGAATTAACGCTCTCCGCGATGCTGACCG 2103
 QY 648 GATTAGCGGTTTGTAGATCGATGATATCAAGATATTAAGATATTTGTGAACGAGT 707
 Db 2102 TGTGCGCGGAGCTGCTGAGTGTGATGCAATCAAGACATTAAGATGTTGTCAACCGAGT 2043
 QY 708 GAGAATGATATGATTAAGAGAGGATATGATGTCAAGTGTGATGTCAGAGAGATTT 767
 Db 2042 GCGGCGAGACTGTGTGAAGGCGGAGGACATGATGTGAGCGCTGACGTGCAAGAAATGCT 1983

QY 768 GGGATGTCTATTCCTTGTGTGTAATTCCTGAAGATTTCTGAGTTATTCGAAGCAGAAATCG 827
 Db 1982 CGGGTGTGCTTTACTAGAGCGGTGTGCGAGAGACACGAGAGTGAATCCGAGATGCAATAG 1923
 QY 828 AGGTTTCCGCTTGTGTCTGAATTAAGCTTCTTAAGCTTGGAGATTTGGCTTTGAGAGC 887
 Db 1922 GGGCGGCGCGGTGTGTGATGATGACCCGCCACGCTCTGCTGTGAGAGAGC 1863
 QY 888 GGGTTGAGAGCTCGTTGAGCAAGATATTAAGGCTTATTTGTGTGAGGA 938
 Db 1862 TACTTGAGATTTGTGTGAAGAAAGATCCGATGACGCGGTATGTGTGAAAG 1812

RESULT 6
 US-10-021-323-6876/c
 / Sequence 6876, Application US/10021323
 / Publication No. US20040123340A1
 / GENERAL INFORMATION:
 / APPLICANT: Deikman, Jill
 / APPLICANT: Feng, Paul C.C.
 / APPLICANT: Fincher, Karen L.
 / APPLICANT: Ziegler, Todd E.
 / TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
 / FILE REFERENCE: 38-21(52274)B
 / CURRENT APPLICATION NUMBER: US/10/021,323
 / CURRENT FILING DATE: 2001-12-12
 / PRIOR APPLICATION NUMBER: US 60/255, 619
 / PRIOR FILING DATE: 2000-12-14
 / NUMBER OF SEQ ID NOS: 17880
 / SEQ ID NO 6876
 / LENGTH: 521
 / TYPE: DNA
 / ORGANISM: Gossypium hirsutum
 / FEATURE:
 / OTHER INFORMATION: Clone ID: LIB3828-011-Q1-N6-D10
 US-10-021-323-6876

Query Match 15.8%; Score 154.2; DB 18; Length 521;
 Best Local Similarity 82.3%; Pred. No. 2.5e-38;
 Matches 177; Conservative 0; Mismatches 38; Indels 0; Gaps 0;
 QY 764 TGTGTGATTCATTCCTTGTGTGTAATTCCTGAAGATTCGAGTTATTCGAAGCAG 823
 Db 521 TGTGTGATTCATTCCTTGTGTGTAATTCCTGAAGATTCGAGTTATTCGAAGCAG 462
 QY 824 ATCGAGGCTTTCGCTTGTCTGAATTAAGCTTCTGAGCTTGGCGGATTTGGCTTTGAGC 883
 Db 461 ACAGAGGGTACCACTTGTCTGAATTAAGCTTCTGAGCTTGGCGGATTTGGCTTTGAGC 402
 QY 884 AGCGGCTTGAAGACTGCTTGAAGCAAGATATGAAGGCTTTATGTCGAGAGAAAG 943
 Db 401 AAGCGCTTGAAGGCTTGTGAAGCAGATATGAAGGCTTTATGTCGAGAGAGAGC 342
 QY 944 CTAGAAACGTGCTTCTTCTTTCTTTTGGCGGC 978
 Db 341 CCAAAAAGCGTGGGTTTCTCATTTTGTGAGGC 307

RESULT 7
 US-10-398-221-8
 / Sequence 8, Application US/10398221
 / Publication No. US20040018514A1
 / GENERAL INFORMATION:
 / APPLICANT: KUNST, Frederick
 / APPLICANT: GLASER, Philippe
 / TITLE OF INVENTION: Listeria innocua, genome and applications
 / FILE REFERENCE: 344 702 - US
 / CURRENT APPLICATION NUMBER: US/10/398,221
 / CURRENT FILING DATE: 2003-03-27
 / PRIOR APPLICATION NUMBER: PCT/FR 01/03 061
 / PRIOR FILING DATE: 2001-10-04
 / PRIOR APPLICATION NUMBER: FR 00/12 697

```
/ PRIOR FILING DATE: 2000-10-04
/ NUMBER OF SEQ ID NOS: 4025
/ SOFTWARE: PatentIn version 3.0
/ SEQ ID NO 8
/ LENGTH: 495269
/ TYPE: DNA
/ ORGANISM: Listeria innocua
/ FEATURE:
/ NAME/KEY: misc feature
/ LOCATION: (1)..(end)
/ OTHER INFORMATION: n can be any nucleotide: a, g, c or t/u
US-10-398-221-8
```

```
Query Match      15.6%; Score 153; DB 17; Length 495269;
Best Local Similarity 53.4%; Pred. No. 3.9e-36;
Matches 355; Conservative 0; Mismatches 295; Indels 15; Gaps 1;
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QY      182 TCGTTATACCTCCGGAAAAGCGGTGTGGAAGAAGACGACAAACACCGGAAATGTCGGTC 241
DB      175073 TAGTCAATTACTCTGGGAAAAGGTGAGTAGGAAAACTTCACTGCTAACTTAGAA 175132
QY      242 TCTCTCTCGCTGTTACGGTTTCTCAGTTGTGCGCACTTACCGCCGACTTGGTCTCCGTA 301
DB      175133 CGGCACTTCTCTTCAAGGTAAAGAGTGTGCTGTGATGATATGATATCGGCTTTCGTA 175192
QY      302 ACCGTGATCTCCTCCAGGGTTAGAGATCGAGTCATTAACCTTGCAGTTCGAGTTATA 361
DB      175193 ATTTAGATGTGTCTTAGAGCTTGAAAATCGATTTATTAATGATTTAGATGATGTTG 175252
QY      362 ACGGAGATTGTGCTCGTTCGATCAAGCTCTGTGTAAGTATAGGTTGGTTCGAAATTCGAA 421
DB      175253 AAGGACGCTGCAAAATCCATCAAGCTATGATTAAGATTAAGGTTTGTATGATTTACTTT 175312
QY      422 TGCCTATGATATCTAACTAGATCGAAACTTCCGATGGGATTTGGTGTAAAGCATTTGG 481
DB      175313 TCTTACTTCCAGCAGACAAACTACGGA-----TAAAAATGCTGTTTCGG 175357
QY      482 AATGCTGTGATGCGTTGAAACCTAGACCGGAAGTTACCGGATTTTCATCATCATCG 541
DB      175358 GAGAACAAATGATAGAGCTAATTAATCAACTACGCTCTGATTAACGATTAATTTCTAATG 175417
QY      542 ATTGTCCTGCAAGAAATCGATGCGCGATTGATTAACCCGCACTTCTCCGGGAAATGAAGCAG 601
DB      175418 ATTGCCCGACAGAAATTTGAACAAGATATAAAAAATCGGTTGCTGAGCTGATTAAGCAA 175477
QY      602 TTCTGTTAACAACCTCCGATATTAACAGCGTTAAAGGATGCTGATAGGGTTAAGGGTTGT 661
DB      175478 TTGTTGTGACTACTCCAGAGATTTTCAGCTGTTGAGATGCGGACAGAAATTAATGCGCTTGC 175537
QY      662 TAGAATGCGATGGAATCAGAGATATTAAGATGATTTGTGAACAGAGTGAACATGATATGA 721
DB      175538 TTGAAAAAAGAGATATTTGAGCCACCAAACTTAATTAATCAATCGTATTCGTACCAATAT 175597
QY      722 TTTAAAGAGAGATATGATGTGCTGATGATGTCGAGAGATGTTGGGATTTGTCATTGC 781
DB      175598 TGGTAATGGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 175657
QY      782 TTGGTGTAAATTCCTGAAGATTTCTGAGATTATTCGAAGCAGATTCGAGGGTTTCCGCTTG 841
DB      175658 TTGGTGTAAATTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 175717
QY      842 TTCTG 846
DB      175718 CGATG 175722
```

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RESULT 8
US-10-398-221-2058/c
; Sequence 2058, Application US/10398221
; Publication No. US20040018514A1
; GENERAL INFORMATION:
; APPLICANT: KUNST, Frederik
; APPLICANT: GLASER, Philippe
```

```
/ TITLE OF INVENTION: Listeria innocua, genome and applications
/ FILE REFERENCE: 344 702 - US
/ CURRENT APPLICATION NUMBER: US/10/398,221
/ CURRENT FILING DATE: 2003-03-27
/ PRIOR APPLICATION NUMBER: PCT/FR 01/03 061
/ PRIOR FILING DATE: 2001-10-04
/ PRIOR APPLICATION NUMBER: FR 00/12 697
/ PRIOR FILING DATE: 2000-10-04
/ NUMBER OF SEQ ID NOS: 4025
/ SOFTWARE: PatentIn version 3.0
/ SEQ ID NO 2058
/ LENGTH: 3011208
/ TYPE: DNA
/ ORGANISM: Listeria innocua
US-10-398-221-2058
```

```
Query Match      15.6%; Score 153; DB 17; Length 3011208;
Best Local Similarity 53.4%; Pred. No. 1.2e-35;
Matches 355; Conservative 0; Mismatches 295; Indels 15; Gaps 1;
```

```
QY      182 TCGTTATACCTCCGGAAAAGCGGTGTGGAAGAAGACGACAAACACCGGAAATGTCGGTC 241
DB      1583882 TAGTCAATTACTCTGGGAAAAGGTGAGTAGGAAAACTTCACTGCTAACTTAGAA 1583823
QY      242 TCTCTCTCGCTGTTACGGTTTCTCAGTTGTGCGCACTTACCGCCGACTTGGTCTCCGTA 301
DB      1583822 CGGCACTTCTCTTCAAGGTAAAGAGTGTGCTGTGATGATATGATATCGGCTTTCGTA 1583763
QY      302 ACCGTGATCTCCTCCAGGGTTAGAGATCGAGTCATTAACCTTGCAGTTCGAGTTATA 361
DB      1583762 ATTTAGATGTGTCTTAGAGCTTGAAAATCGATTTATTAATGATTTAGATGATGTTG 1583703
QY      362 ACGGAGATTGTGCTCGTTCGATCAAGCTCTGTGTAAGTATAGGTTGGTTCGAAATTCGAA 421
DB      1583702 AAGGACGCTGCAAAATCCATCAAGCTATGATTAAGATTAAGGTTTGTATGATTTACTTT 1583643
QY      422 TGCCTATGATATCTAACTAGATCGAAACTTCCGATGGGATTTGGTGTAAAGCATTTGG 481
DB      1583642 TCTTACTTCCAGCAGACAAACTACGGA-----TAAAAATGCTGTTTCGG 1583598
QY      482 AATGCTGTGATGCGTTGAAACCTAGACCGGAAGTTACCGGATTTTCATCATCATCG 541
DB      1583597 GAGAACAAATGATAGAGCTAATTAATCAACTACGCTCTGATTAACGATTAATTTCTAATG 1583538
QY      542 ATTGTCCTGCAAGAAATCGATGCGCGATTGATTAACCCGCACTTCTCCGGGAAATGAAGCAG 601
DB      1583537 ATTGCCCGACAGAAATTTGAACAAGATATAAAAAATCGGTTGCTGAGCTGATTAAGCAA 1583478
QY      602 TTCTGTTAACAACCTCCGATATTAACAGCGTTAAAGGATGCTGATAGGGTTAAGGGTTGT 661
DB      1583477 TTGTTGTGACTACTCCAGAGATTTTCAGCTGTTGAGATGCGGACAGAAATTAATGCGCTTGC 1583418
QY      662 TAGAATGCGATGGAATCAGAGATATTAAGATGATTTGTGAACAGAGTGAACATGATATGA 721
DB      1583417 TTGAAAAAAGAGATATTTGAGCCACCAAACTTAATTAATCAATCGTATTCGTACCAATAT 1583358
QY      722 TTTAAAGAGAGATATGATGTGCTGATGATGTCGAGAGATGTTGGGATTTGTCATTGC 781
DB      1583357 TGGTAATGGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1583298
QY      782 TTGGTGTAAATTCCTGAAGATTTCTGAGATTATTCGAAGCAGATTCGAGGGTTTCCGCTTG 841
DB      1583297 TTGGTGTAAATTTATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1583238
QY      842 TTCTG 846
DB      1583237 CGATG 1583233
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RESULT 9
US-10-424-599-76259
; Sequence 76259, Application US/10424599
; Publication No. US20040031072A1
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Query Match	14.9%	Score 145.4	DB 17	Length 406
Best Local Similarity	75.0%	Pred. No. 1.4e-35		
Matches 195	Conservative 0	Mismatches 62	Indels 3	Gaps 1
QY	718	ATGATTTAAGAGAGAGATATGATGTCAGTGTAGATGTGCAGAGATGTTGGATTGCA	777	
Db	2	ATGAGCAAAAAGGAGAGCCATCATTTTGGTGTTGAGCGGGCAAAAATGTTAGGTTGCCCT	61	
QY	778	TTCGTTGGTGTTAATTCCTGAGATTCCTAGGTTATTCGAAGCAGATCGAGGGTTTCCG	837	
Db	62	TTCGTCGGGGTTATTCCTGAGATAGTAGGTTATTAAAGCCCAATAGAGGTTTCCCT	121	
QY	838	CTTGTTTCGATTAAGCCTTCCTACGCTTGCGGATTTGGCGTTTGACAGCGCGCTTGAGAG	897	
Db	122	CTTGTCCTCAACAGCCCTCCACCTTTGGCCCGATTTGGCGCTTGCAACAACCGCGTGAAG	181	
QY	898	CTCGTTGAGCAAGATAGATGAAGGCTTTATGTGTGAGAGAAAGAACTAAGAAACGTGGC	957	
Db	182	CTCGTGGAGCAAGATAGATGATCAAGCGCTGGTGTGTGAAGAACAAAC--CAACGTGGG	238	
QY	958	TTCCTCTCTCTCTTTGGCGG	977	
Db	239	TTTTTCTCTTTTGTGGTG	258	

Query Match	13.5%	Score 132.4	DB 18	Length 547
Best Local Similarity	61.1%	Pred. No. 2,6e-31		
Matches	214	Conservative 0	Mismatches 136	Indels 0
Y	151	CCGGAACTGCCCGAGAAACGCCGATCGTGGTATCACCTCCGAAAGGCGGTGT	210	
b	198	CCGAACTCTCGGGCCCGAACCCCGCGCTGGTGTGTCACTCCGGAGAAAGCGCGTC	257	
Y	211	GGAAAGAGCAACAACCCGAATGCGGTCTCTCTCGCGCTGTACGGTTTTCAGTT	270	
b	258	GGCAAGACCACCAACCGCGCAACTCGCGCGCTCGCTCGCGCGCTTAATTCGCCGCC	317	
Y	271	GTGCGCATTAGAGCGGCACTTGTGTCTCCGTAACTCTGAATCTCTCTAGGGTTAGAAAT	330	
Y	318	GTGCGCGTGAAGCGCCGACGCGGCGCTCCGCAACTCGACTCTGTCTCGGCTCGAGAAC	377	
b	331	CGAGTCATTTACACTTGGGTGAGGTTTAAACGAGAGATTGCTCTGATCAAGCTGTG	390	
Y	378	CGCGTCACTCAACCGCGCGGACGTACTCGCGCGGAGCTGAGGCTGACCAAGCGCTC	437	
b	391	GTACGTGATTAAGCGTTGTGCAATTTGCAATTGCTATGTATATCTAAACCTAGATCGAA	450	
Y	438	GTCCGACACCGCGCGCTCCAGACTTCACTTCTGCTCTTCCAAAGCCCGGCTCCAG	497	


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COMPUTER READABLE FORM:
MEDIUM TYPE: CD-ROM ISO9660
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: Windows NT 4.0
SOFTWARE: UNIX
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/335,977
FILING DATE: 30-Dec-2002
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/993,002
FILING DATE: 17-Dec-1997
ATTORNEY/AGENT INFORMATION:
NAME: Mandragoras, Amy E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: GTN-018
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)742-4214
INFORMATION FOR SEQ ID NO: 3900:
SEQUENCE CHARACTERISTICS:
LENGTH: 807 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Helicobacter pylori
FEATURE:
NAME/KEY: misc_feature
LOCATION: (B) LOCATION 1...807
SEQUENCE DESCRIPTION: SEQ ID NO: 3900:
US-10-335-977-3900

Query Match      8.3%; Score 81.4; DB 17; Length 807;
Best Local Similarity 49.1%; Pred. No. 7,8e-15;
Matches 337; Conservative 0; Mismatches 311; Indels 39; Gaps 3;

QY 179 TCGTCGTTACACCTCCGGAAGGCGGTGTGGAAGACGACACCGCAATGTCG 238
DB 11 TAGTACTATACCTTAGGGAAGGGGCGTGGCAAAACACACACGCGCTAATTAG 70
QY 239 GTCCTCTCTCGCTGCTTACGTTTCTCAGTTGTGCGCATGACGCGCACTTGCTCC 298
DB 71 CGATTGGCTTGGCTGAGAGCGGTAAAGAGTGTGAGCGGTGATTGTCATAGCCCTTA 130
QY 299 GTAACCTGATCTCCCTTAGGGTTAGAGATCGATCAATTACACTTGCCTGAGGTTA 358
DB 131 GGAACCTGACATGATTTTAGGCTTAGAAATCGCATTTGATGATGTGTGAGATGTA 190
QY 359 TAAACGGAATGTGCTCTCGATCAAGCTCTGTAGTGAAGGCTTGTCGATTTTCG 418
DB 191 TGAATAAAATTCACACCTTTCACAGGCTTTGATCAGATTAAGAAAGATAAAACCTTT 250
QY 419 AATTGTATATATATCTAACTAGATGAAACCTTCCATGGAATTTGTTGATGAAGCAT 478
DB 251 CTTTTCACGGCCCTCACAAAGTAAGATAA-----AATATTTTAGATA 295
QY 479 TGAATGCGCTTGTGATGCGTGAAGAACCTAGACCGGAAGTTACCGGATTTTCATCA 538
DB 296 AGGAAAAGTACGATTTTAATCAACGCTTTTAGGGCGGATTTT--GACTATATTTTGA 352
QY 539 TCGATTGTCCTGAGGAATCGATGCGGATTCATTAACCGCATTAATCCGCGAATGAG 598
DB 353 TTGACTCACCGGCTGGGATGMAAGCGGTTTGAAGCATGCAATTTTGTATCGGACATGG 412
QY 599 CAGTTCGTGTAACAACCTCCGATATAACAGCGTTAAGGATGCTGATAGGGTTACGGGTT 658
DB 413 CGTTAGTGTGTAAAGCGCGAAGTAGATTCCTTAAGGATAGCAGAGAGTGAATGGCA 472
QY 659 TGTTAG-----AATCGATGGAATCAGAGATTAAGATGATTTG 697

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DB 473 TTATGACGGAAGTCTAATCGGGCCAAAAGTGGGGAAGAAGTGCATAGCATTTGATA 532
QY 698 TGAACAGATGAGAACTGATATGATTAAGAGAGAGATTGATGTCAGTGTAGATGTC 757
DB 533 TCATGCTTAAACCTGAGTAGTGCCAAATGGGAGATGATTTCCATAGAAAGATGC 592
QY 758 AGGAGATGTTGGATTCATTCATTCGTTGTTGTTATTCCTGGAAGATTCTGAGTTATTCGA 817
DB 593 TTAAATCTTGTGCTTGCCCTTTAATTGGGATCATTCCTGAGATCACCATATTTATTCAG 652
QY 818 GACGATGAGAGGTTTCGCTTTC 844
DB 653 CCAACAAATAAGGCGAGCGGTGATTC 679

RESULT 15
US-10-672-787-13/C
Sequence 13, Application US/10672787
Publication No. US2004006755A1
GENERAL INFORMATION:
APPLICANT: LAGACE, Robert, R.
APPLICANT: PATTERSON, Chandra
APPLICANT: BERG, Kim, L.
TITLE OF INVENTION: NUCLEOTIDE SEQUENCES OF MORAXELLA CATARRHALIS GENOME
FILE REFERENCE: ELITRA.025C1
CURRENT APPLICATION NUMBER: US/10/672,787
CURRENT FILING DATE: 2003-09-26
PRIOR APPLICATION NUMBER: 09/596,002
PRIOR FILING DATE: 2000-06-16
NUMBER OF SEQ ID NOS: 41
SOFTWARE: PERL Program
SEQ ID NO 13
LENGTH: 31940
TYPE: DNA
ORGANISM: Moraxella catarrhalis
US-10-672-787-13

Query Match      7.5%; Score 73; DB 17; Length 31940;
Best Local Similarity 54.2%; Pred. No. 3.6e-11;
Matches 148; Conservative 0; Mismatches 125; Indels 0; Gaps 0;

QY 178 ATGCTGTTATACCTCCGGAAGGCGGTGTGGAAGACGACACACCGCAATGTC 237
DB 273 ATGCTGTTATGTAAGTGAAGGCGGTGTGGAAGACGACACACCGCAATGTC 214
QY 238 GGTCTCTCTGCTGCTTACGTTTCTCAGTTGTGCGCATGACGCGCACTTGCTC 297
DB 213 GTGCAAGGCTTGTCTAAGCGTGTGTTAAACAGTATCATGATTTGATGCGGTTG 154
QY 298 CGTAACCTGATCTCCCTTAGGGTTAGAGATCGAGTCAATTACACTTGCCTGAGGTT 357
DB 153 CGTATTTATATCTAATTAATGAGGTGTGAAACGATGCTATATGACTTTTGAAGTGTG 94
QY 358 ATAAACGGAATGTGCTCTCGATCAAGCTCTGTAGTGAAGTGAAGGTTGTGGAATTTTC 417
DB 93 ATCAGGTGTAATCCAAAGCTTGCTCAAGCTTATGTAAGACAAACAAATTTGAAAAATCTA 34
QY 418 GAATTCATATATATCTAACTAGATGAAA 450
DB 33 TACATTTTTCCTGATCGCAACGCGAGCAAA 1

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Search completed: March 10, 2005, 23:46:33
Job time : 618 secs